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                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=20545237; PubMed=11093171;

DOI=10.1002/1521-4141(2000012)30:12<3516::AID-IMMU3516>3.0.CO;2-S;

Matesanz F., Delgado C., Fresno M., Alcina A.;

"Allelic selection of human IL-2 gene.";

Eur. J. Immunol. 30:3516-3521(2000).

EMBL; AF228636; AAG53575.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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P605563; P01585;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TGGF) (Aldesleukin).
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Taniguchi I., Matsui H., Pujita I., Takaoka C., Kashima N.,
Yoshimoto R., Hamuro J.;
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                       GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0006955; P:immue response; IEA.
InterPro; IPR009079; 4 halix cytokine.
InterPro; IPR000779; Interleukin-2.
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Pred. No. 5.1e-14;
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                                                 Created)
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PRINTS, PR00265; INTERLEUKIN2.
ProDom, PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
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                                                                  01-MAR-2004 (TrEMBLrel. 26, Interleukin-2 (Fragment).
                                               (TrEMBLrel. 17, (TrEMBLrel. 17,
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Best Local Similarity 100.
Matches 30, Conservative
                           PRELIMINARY;
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                                                                                       Homo sapiens (Human)
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                                                                                                                    NCBI_TaxID=9606;
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MEDLINE=4012019 (pubmed=6112994, Meads 12.094)

Meads A. Mishino N. Obsar N. Mita S., Nomiyama H., Shimada K., Mara S. Wandlano N., Teranishi T. Mishino N., Obsar N., Mishino N., Obsar N., Mishino N., Obsar N., Mishino N., Data N., District N.
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proliferation and other activities crucial to regulation of the
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                                                                                                                                                                                                                            SEQUENCE OF 1-69 FROM N.A.
MEDLINE-87064618; PubMed=3491296;
Siebenlist U., Durand D.B., Bressler P., Holbrook N.J., Norris C.A.,
Kamoun M., Kant J.A., Crabtree G.R.;
"Promoter region of interleukin-2 gene undergoes chromatin structure
changes and confers inducibility on chloramphenical acetyltransferase
gene during activation of T cells";
Mol. Cell. Biol. 6:3042-3049(1986).
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                                                                                         MEDLINE-89062420; PubMed-3264184;
Weir M.P., Chaplin M.A., Wallace D.M., Dykes C.W., Hobden A.N.;
"Structure-activity relationships of recombinant human interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-85038540; PubMed-6333684;
Robb R.J., Kutny R.M., Panico M., Morris H.R., Chowdhry V.;
"Amino acid sequence and post-translational modification of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 21-153, DISULFIDE BOND, AND CARBOHYDRATE-LINKAGE SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-90008901; PubMed-2793860;
Conradt H.S., Nimtz M., Dittmar K.E.J., Lindenmaier W., Hoppe J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-68 FROM N.A.
Nishino N., Obaru K., Maeda S., Shimada K., Onoue K.;
"Organization of the DNA regions flanking the human interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modelling.";
Structure 2:839-851(1994).
-!- FUNCTION: Produced by T-cells in response to antigenic or
    mitogenic stimulation, this protein is required for T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mott H.R., Driscoll P.C., Boyd J., Cooke R.M., Weir M.P., Campbell I.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brandhuber B.J., Boone T., Kenney W.C., McKay D.B., "Three-dimensional structure of interleukin-2.", Science 238:1707-1709(1987).
                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE=88070646; PubMed=3500515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92335891; PubMed=1631562;
Bazan J.F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biomed. Res. 6:197-205(1985).
                                                                 SEQUENCE OF 21-153 FROM N.A
mouse cDNA sequences.";
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CCCCLLTRAY BREET B
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Immune response. Can similate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.

-!- SUBCELLULAR LOCATION: Secreted.
-!- DISEASE: Involved in a form of T-cell acute lymphoblastic leukemia (T-ALL) by a chromosomal translocation t(4,16) (q26;p13) which involves TYRESF17 and IL2.
-!- PHARMACEUTICAL: Available under the name Proleukin (Chiron). Used in patients with renal cell carcinoma or metastatic melanoma.
-!- SIMILARITY: Belongs to the IL2 family.
-!- DATABASE: NAME=RkD Systems. cytokine source book: IL2;
-!- DATABASE: NAWE-RkD Systems.com/asp/g_sitebuilder.asp?bodyId=206".
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Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
NCBI_TaxID=9580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IL2 HYLLA STANDARD; PRT; 153 AA.
P6056; P01585;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 147; DB 1;
100.0%; Pred. No. 5.2e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 APTSSSTKKTQLQLEHLLLDLQMILNGINN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J00264; AAD48509.1; -.
EMBL; X01586; CAA25742.1; -.
EMBL; V00564; CAA23827.1; -.
EMBL; X00695; CAA2529.1; -.
EMBL; K02056; AAA98792.1; -.
EMBL; M13879; AAA59141.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hylobates lar (Common gibbon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=IL2;
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InterPro; IPR000779; Interleukin-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=IL2;
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            r-cell.
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                                                                                                                                                                                                                                                              Matches
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       8
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TISSUBECE FROM N.A.

TISSUBECE, rescued clones;

MEDLINE=223825; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=223825; PubMed=124.7932; DOI=10.1073/pnas.242603899;

A trausberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

A phokins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B piatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B piatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B comparein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B romatein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,

R and S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,

R Richards S., Mochey K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

M. Maring M.J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"And Mana A., Morley W. Morley R.M., Butterfield Y.S.,

"A monte S.J., Marra M.A.,

"A mones S.J., Marra M.A.,

"A mones S.J., Marra M.A.,

"A mones C.J., Marra M.D.,

"A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                By similarity.
Interleukin-2.
O-linked (GalNAc. . .) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                    InterPro; IPR000729; Interleukin-2.
Pfam; PF00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
Prodom; PD003649; Interleukin-2; 1.
SWART; SW00189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
CYtokine; Glycoprotein; Growth factor; Immune response; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                       By similarity.; 59E2F40F25860F84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, BC066254, AAH66254.1, -...

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005134; F:interleukin-2 receptor binding; IEA.

GO; GO:0006555; P:immune response; IEA.

InterPro; IPR009079; 4_helix_cytokine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 147; DB 1;
Pred. No. 5.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 APTSSSTKKTÓLOLEHLLLDLÓMILNGINN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-UUL-2004 (TrEMBLrel. 27, Created) 05-UUL-2004 (TrEMBLrel. 27, Last seq 05-UUL-2004 (TrEMBLrel. 27, Last ann
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                                                                                                                                                                                                                                                                                                                                                         125 B
17628 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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TISSUE=PCR rescued clones;
Strausberg R.;
                            EMBL; M11144; AAA35454.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
es 30; Conservative
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                                                                                                                                                                                                                                                                                   20
153
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78
153 AA;
                                                    PIR; A94067; ICGI2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin 2,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=IL2;
                                                                                                                                                                                                                                                                                                                                                         DISULPID
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                      T-cell.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

TISSUE-Peripheral blood;

Yabe M., Matsuura Y., Tatsumi M.;

Submitted (JUL-1995) to the EMEL/GenBank/DDBJ databases.

-!- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells (By
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
Prodom, PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
                                                                                                                                                                                                             Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 154;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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O-linked (GalNAc. . .) (By
PEAM; PP00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
ProDom, PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
PROSITE; PS000424; INTERLEUKIN 2; 1.
SRQUENCE 153 AA; 17597 MW; 1942F50F25960E88 CRC64;
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7853FE624A5E4A49 CRC64;
                                                                                                                                                                                                       100.0%; Score 147; DB 2;
100.0%; Pred. No. 5.2e-14;
trive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 147; DB 1;
100.0%; Pred. No. 5.2e-14;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the IL-2 family.
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                                                                                                                                                                                                                                                                                                                            1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
                                                                                                                                                                                                                                                                                                                                                             21 APTSSSTKKTQLQLEHLLLDLQMILNGINN
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InterPro; IPR000779; Interleukin-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17686 MW;
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                                                                                                                                                                                                                                                                   30; Conservative
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Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecinae; Macaca.
NCBI_TaxID=9541;
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23
126
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                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                 J. Immunol. 155:3946-3954(1995).

-!- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokineactivated killer cells, natural killer cells, and glioma cells (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           By similarity.
Interleukin-2.
O-linked (GalNac. . .) (By similarity).
6 SAEBA480F204BA49 CRC64;
                                                                                                            Macaca nemestrina (Pig-tailed macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Last sequence update)
6-JUL-2004 (Rel. 44, Last annocation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
Name=IL2; Synonyms=IL-2;
Papio annis (Olive baboon).
Eukaryotausi Metazoa; Mordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarthini; Cercopithecidae;
                                                                                                                                                                                                                                                                                            Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
"Comparative sequence analysis of cytokine genes from human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 147; DB 1;
Pred. No. 5.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR000779; Interleukin-2.
                                                                                                                                                                                                                                                                       MEDLINE=96003435; PubMed=7561102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last seqn
05-JUL-2004 (Rel. 44, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00265; INTERLEUKIN2.
SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 AA; 17685 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U19852; AAA86714.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                             Cercopithecinae; Macaca.
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154
23
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                                                                                                                                                                                                                                                                                                                                     nonhuman primates."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P01585; 1M48.
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                              NCBI_TaxID=9545;
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23
78
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Local Sir.
30;
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Q865Y1;
                                                                                                Name=IL2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       By similarity.
Interleukin-2.
O-linked (GalNAc. ..) (By similarity)
By similarity.
                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A. "Comparative sequence analysis of cytokine genes from human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                             PRT; 134 An.
P68291; P51498;
01-0CT-1996 (Rel. 34, Created)
01-0CT-2996 (Rel. 34, Last sequence update)
25-0CT-2094 (Rel. 45, Last amnotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6AEBA480F204BA49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 147; DB 1;
100.0%; Pred. No. 5.2e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
--- SUBCELLULAR LOCATION: Secreted.
--- SIMILARITY: Belongs to the IL-2 family.
                  1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
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                                        21 APTSSSTKKTOLOLEHLLLDLOMILNGINN
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InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR000779; Interleukin-2.
Pfan; PF00715; IL2; 1
PRINTS; PR00265; INTERLEUKIN2.
SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Blood;
MEDLINE=96003435; Pubmed=7561102;
                                                                                                                                                                                                                                                                                        Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17685 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
nes 30; Conservative
                                                                                                                                                                                                                                                                                                                                                   Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
154
23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nonhuman primates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9544;
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SOUTH THE TRANSPORT OF THE TRANSPORT OF

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Gaps

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154 AA

PRT;

STANDARD;

IL2 MACNE

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Matches

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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . .) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A., Patarroyo M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aotus lemurinus (Northern gray-necked night monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 145; DB 1; Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.6%; Score 145; DB 2; Length 154; 96.7%; Pred. No. 1e-13; ive 1; Mismatches 0; Indels
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EMBL; U88364; AAD41534.1; -.
GO; GO:0005576; C:extracellular; IRA.
GO; GO:0005134; F:interleukin-2 receptor binding; IRA.
GO; GO:0006955; P:immune response; IRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 20 By similarity.
21 154 Interleukin-2.
78 126 By similarity.
23 23 O-linked (GallMac. . .) (By
154 AA; 17657 MW; AA642BABBCA87569 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB752ABBADA96469 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                             -!- SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 AA
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InterPro; IPR000779; Interleukin-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytokine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0265; INTERLEUKINZ.
ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR009079; 4 helix cytoki
InterPro; IPR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
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PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
SWART; SM00189; 11.2; 1.
SROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 154 AA; 17675 MW; AB75.
                                                                                                           SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF294755; AAK92042.1; -.
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Les 29, Conserv
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                                                                        similarity)
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Best Local S
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SIGNAL
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Matches
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SOUTH THE WARRANT THE TENT OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                        immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia, Eutheria, Primates, Platyrrhini, Cebidae, Cebinae, Saimiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (By similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodom; PD003649; Interleukin-2; 1.
SMART; SM00189; ILL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 147; DB 1; Length 154;
; Pred. No. 5.2e-14;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47F486BDF204AD6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    By similarity.
O-linked (GalNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
Interleukin-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 APTSSSTKKTQLQLEHLLLDLQMILNGINN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monkey)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P01585; 1M49.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saimiri sciureus (Common squirrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AY234220; AAO85333.1; -.
                                                                                                                                                                            'Nonhuman primate cytokines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17713 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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nes 30; Conservative
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154
126
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                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                          NCBI_TaxID=9555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9521;
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78
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SIGNAL
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Aotus nancymaae (Ma's night monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
NCBI_TaxID=37293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
Patarroyo M.E.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muīillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A., Patarroyo M.E., Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Papio hamadryas (Hamadryas baboon). 's butebrata; Buteleostomi; bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butheria; Primates; Catarrhini; Cercopithecidae; Cercopithecidae;
                                                        Score 145; DB 2; Length 154;
Pred. No. 1e-13;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.6%; Score 145; DB 2; Length 154; 96.7%; Pred. No. 1e-13; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000779; Interleukin-2.
Pfam; PR00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
PROD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN_2; 1.
SROURNCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;
154 AA; 17675 MW; AB752ABBADA96469 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U88361; AAD41535.1; -. GO; GO:0005576; C:extracellular; IEA. GO; GO:0005134; F:interleukin-2 receptor binding; IEA. GO; GO:0006955; P:immune response; IEA. InterPro; IPR009079; 4 helix cytokine. InterPro; IPR000779; InterPukin-2.
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HSSP; P60568; IIRL.
GO: 000105576; C:extracellular; IEA.
GO: GO:0005514; F:interleukin-2 receptor binding; IEA.
GO: GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                  154 AA
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                                                                                                                                                                                                             21 APTSSSTKKTQLQLEHLLLDLQMLLNGINN 50
                                                                                                                                                                              1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
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                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                        98.6%;
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 96.7
Matches 29, Conservative
                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                  Local Similarity
les 29; Conserv
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SEQUENCE
                                                     Query Match
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Q7JFM5
                                                                                                                     Matches
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Batarroyo M.E.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; UB8362; AAD41537.1;
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:000555; P:immune response; IEA.
InterPro; IPR0090779; 4 helix cytokine.
InterPro; IPR0090779; Interleukin-2.
Pfam; PF00715; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     korub nigytrceps (Black-Readed Owl monkey).
Bukaryota, Metazoa, Chorodata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Platyrrhini, Cebidae, Aotinae, Aotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Mullilo.L., Hernandez B., Echeverry S.J., Mendez J.A., Moreno A., Patarroyo M.E., Hernandez B., Echeverry S.J., Mendez J.A., Moreno A., Butarroyo M.E., Hernandez B., EMBL/GenBank/DDBJ databases.
EMBL; U88363; AAD41536.1;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 98.6%; Score 145; DB 2; Length 154; Local Similarity 96.7%; Pred. No. 1e-13; nes 29; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONTROL OF THE STATE OF THE STATE OF THE STATE OF CONTROL OF CONTR
                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                       154 AA
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                      1 APTSSSTKKTOLOLEHLLLDLOMILNGINN 30
                                                     21 APTSSSTKKTQLQLEHLLLDLQMLLNGINN 50
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                                                                                                                                                                                                                                                                                                                                                                                                                  Actus nigriceps (Black-headed owl monkey)
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ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN_2; 1.
                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=57175;
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HSSP; P60568; 11RL
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SIGNAL
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P46649;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                      98.6%; Score 145; DB 2; Length 154; 96.7%; Pred. No. 1e-13;
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                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chikara S.K., Sharma G.;
Chikara S.K., Sharma S.K., S
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY283686; AAP35033.1; --
InterPro; IPR009079; 4 helix cytokine.
InterPro; IRR000779; Interleukin-2.
Pfam; PP00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
PROSITE; S000189; IL2; 11.2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
SRQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 133 AA; 15462 MW; 1699F680A09DB3B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Pred. No. 1.8e-13;
                                                                                                                                                                                       Pred. No. 1e-13;
1; Mismatches
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100.0%; Pred. No. 1...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          133 AA
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                                                                                                                                                                                                                                             1 APTSSSTKKTOLOLEHLLLDLOMILNGINN 30
                                                                                                                                                                                                                                                                21 APTSSSTKKTQLQLEHLLLDLQMLLNGINN 50
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ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
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                                                                                                                                                                                       Best Local Similarity 96.7
Matches 29; Conservative
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Best Local Similarity
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Interleukin-2.
O-linked (GalNAc. .) (By similarity).
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-!- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.
-!- SUBCELULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=IL2;
Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A., "Comparative sequence analysis of cytokine genes from human and nonhuman primates.";
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Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
                                                                                                                                                                                                                                                                                                                                                             Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IRR003079; 4 helix cytokine.
InterPro; IRR003079; 4 helix cytokine.
InterPro; IRR003079; Interleukin-2.
Pfam; PF00715; IL2; 1.
ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
SRQUENCE 133 AA; 15461 MW; 1699FEA880959B90 CRC64;
                                                                                                                                                                                                                                                                                                                                                          Score 143; DB 2; I
Pred. No. 1.8e-13;
                                                                                                                                                                                                                                                                                                                                   97.3%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PTSSSTKKTQLQLEHLLLDLQMILNGINN 30
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InterPro; IPR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
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ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
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01-NOV-1995 (Rel. 32, Last seq
05-JUL-2004 (Rel. 44, Last ann
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154
23
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23
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1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
                                                                                                                                                            Interleukin 2.
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01-MAR-2004
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                                                                                             Q13169
Q13169;
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                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A Mischen E.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenco L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,
A Scares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mitting M., Andan A., Young A.C., Shevchenko Y., Bouffard G.G.,
McIrywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
T "Generation and initial analysis of more than 15,000 full-length human
                                                                                             ö
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                  Homo Sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                            0;
                                                               Query Match 96.6%; Score 142; DB 1; Length 154; Best Local Similarity 96.7%; Pred. No. 3e-13; Matches 29; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 93.2%; Score 137; DB 2; Length 15
Best Local Similarity 96.7%; Pred. No. 1.7e-12;
Matches 29; Conservative 0; Mismatches 1; Indels
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25 25 R -> S.
74 74 K -> B.
154 AA; 17754 MW; 9FBB51814204BA48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         00424; INTERLEUKIN_2; 1.
153 AA; 17644 MW; 59F9980409964F84 CRC64;
                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                              153 AA
                                                                                                                    1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
                                                                                                                                       21 APTSRSTKKTQLQLEHLLLDLQMILNGINN 50
                                                                                                                                                                                                             PRT;
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PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
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PROSITE; PS00424; INTERLEUKIN 2;
SEQUENCE 153 AA; 17644 MW; 55
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                           nterleukin 2,.
             VARIANT
VARIANT
SEQUENCE
  DISULPID
                                                                                                                                                                                                                          Q6NZ91;
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Q6NZ91
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Xu D., Wu Y., Chen J., Yu L., Zhong M., Hui Y., Qu H.;
"Expression of human IL-2 from gene transferred mouse melanoma cells and its effect on the growth of mouse melanoma.";
Chin. J. Microbiol. Immunol. 13:78-82(1993).
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                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005576; C:extracellular; TAS.
GO; GO:0005134; F:interleukin-2 receptor binding; TAS.
GO; GO:0005134; F:kinase activator activity; TAS.
GO; GO:000516; P:kinase activator activity; TAS.
GO; GO:000516; P:atil-apoptos18; TAS.
GO; GO:000555; P:immune response; TAS.
GO; GO:000555; P:immune response; TAS.
GO; GO:001010; P:natural killer cell activation; TAS.
GO; GO:001010; P:posttive regulation of cell growth; TAS.
GO; GO:0010284; P:posttive regulation of cell proliferation; TAS.
GO; GO:0000284; P:posttive regulation of cell proliferation; TAS.
InterPro; IPR000779; Interleukin-2.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu L.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD003649; Interleukin 2; 1.
SWART; SW0189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 156 AA; 18002 MW; BE0452D43B336389 CRC64;
                                                                                                                                                                                                                      (TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
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                                                                                                                                                 156 AA
21 ALTSSSTKKTQLQLEHLLLDLQMILNGINN 50
                                                                                                                                                                                                 Created)
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                                                                                                                                                 PRT;
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PRINTS; PR00265; INTERLEUKIN2.
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01,
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                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Pinnipedia, Phocidae, Mirounga.
          Eizenberg O., Faber-Elman A., Lotan M., Schwartz M.;
"Interleukin-2 transcripts in human and rodent brains: possible
                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TGGF)
                                                                                                                                                                                                                       Length 139;
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                  139 AA; 15986 MW; 731FBA406D0C63C5 CRC64;
                                                                       GO, GO: 0005576; C:extracellular; IEA.
GO; GO: 0005134; F:interleukin-2 receptor binding; IEA.
GO; GO: 0005134; F:interleukin-2 receptor binding; IEA.
GO; GO: 0005576; P:immune response; IEA.
InterPro; IPR000579; J. 4helix cytokine.
InterPro; IPR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
PRINTS; PR001565; INTERLEUKIN2.
PRODOM; PD003649; Interleukin-2; 1.
                                                                                                                                                                                                                     91.2%; Score 134; DB 2; L. 93.3%; Pred. No. 4.3e-12; ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                      Mirounga angustirostris (Northern elephant seal).
                                                                                                                                                                                                                                                                                                                                            154 AA

    SUBCELLUTAR LOCATION: Secreted.
    SIMILARITY: Belongs to the IL-2 family.

                                                                                                                                                                                                                                                                1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
                                                                                                                                                                                                                                                                               17 APTSSSTKKTQLXLEHLLLDLQMILXGINN 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
PRODOM; PD003649; Interleukin-2; 1.
SWART; SM00189; IL2; 1.
                                                                                                                                                                        PROSITE, PS00424; INTERLEUKIN 2; 1.
                                                                                                                                                                                                                                                                                                                                           PRT;
                                 expression by astrocytes.";
J. Neurocohem. 64.1928-1936(1995).
EMBL; 877835; AAD14264.1; -.
HSSP; P60568; 1IRL.
MEDLINE=95239150; PubMed=7722480;
                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U79187; AAC12258.1; -
                                                                                                                                                                                                                Query Match
Best Local Similarity 93.3*
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                       139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P01585;
                                                                                                                                                                                                                                                                                                                                         11.2 MIRAN
062641;
                                                                                                                                                                                                                                                                                                                                                                                                         Name=IL2;
                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=93356765; PubMed=8352761;
Cozzi P.J., Padrid P.A., Takeda J., Alegre M.-A., Yuhki N., Leff A.R.;
"Sequence and functional characterization of feline interleukin 2.";
                                                                                                                                                                                                                              Gaps
                                                                                                   . .) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Felis silvestris catus (Cat).
Sukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEUKIN 2; 1.
Growth factor; Immune response; Signal;
PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
05-JUL-2004 (Rel. 44, Last amoutation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TGGP)
                                                                                                                                                                                     Length 154;
                                                                                                                                                                                 Score 116; DB 1; Length 15
Pred. No. 2.6e-09;
6; Mismatches 2; Indels
                                                                                                                                              0C92337A4B16B6BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 194:1038-1043(1993).
                                                                                Interleukin-2.
O-linked (GalNAc.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
Interleukin-2.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                    154 AA
                                                          By similarity
                                                                                                                                                                                                                                                                        1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                             21 APTISSTKETQQQLEQLLLDLRLLLNGVNN
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HSSP; P01585; 1M49.
Interpro; IPR009079; 4 helix cytokir
Interpro; IPR000779; Interleukin-2.
Pfam; PP00715; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                              154 AA; 17661 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00424; INTERLEUKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L19402; AAA02865.1; -.
EMBL; L25408; AAA51431.1; -.
                                                                                                                                                                                     78.9%;
                                                                                                                                                                                                       l Similarity 73.3%;
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                            20
154
23
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154
126
                                                                                                                                                                                                       Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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78
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01-0CT-1994
               Cytokine; (
T-cell.
                                                                                                                                                                                                                                                                                                                                                                                                                  11.2 FELCA
Q07885;
                                                                                                   CARBOHYD
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
DISULFID
                                                                                                                                                                                   Query Match
                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -cell.
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                                                                                    CHAIN
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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112_CANFA
115_JU2_C
AC 122_C
AC 122_C
AC 122_C
AC 125_JU
DT 15_JU
DT 15_JU
DF 15_JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99221046; PubMed=10206205; DOI=10.1016/S0165-2427(99)00009-4; St-Laurent G., Beliveau C., Archambault D.; Sterlaurent G., Beliveau C., Archambault D.; Molecular cloning and phylogenetic analysis of beluga whale (Delphinapterus leucas) and grey seal (Halichoerus grypus) interleukin
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Halichoerus grypus (Gray seal).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Pinnipedia, Phocidae, Halichoerus.
N-linked (GlCNAc. .) (Potential).

KI -> RM (in Ref. 2).

F -> I (in Ref. 2).

; 2E71E3BD8B9665EF CRC64;
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                                                                                                                                                             Length 154;
                                                                                                                                                       Query Match 77.6%; Score 114; DB 1; Length 15
Best Local Similarity 73.3%; Pred. No. 5.2e-09;
Matches 22; Conservative 5; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS: PROOSS; INTERLEUKINZ.
PRODOM; PD003649; Interleukin-2; 1.
SMART; SM00189; ILL2; 1.
PROSITE; PRO0424; INTERLEUKIN 2; 1.
SRQUENCE 155 AA; 17860 MW; F18F449AC672241A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR009709; 4 helix_cytokine.
InterPro; IPR00779; Interleukin-2.
PRO0715; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
11-JUNAR-2004 (TrEMBLrel. 26, Last annotation update)
Interleukin 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 73.8%; Score 108.5; DB 2; Best Local Similarity 74.2%; Pred. No. 3.6e-08; Matches 23; Conservative 5; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vet. Immunol. Immunopathol. 67:385-394(1999)
EMBL; AF072871; AAD40848.1; -.
HSSP; P60568; IIRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 APTISSSTKETQQQLEQLLLDLRLLLNGVNN 51
                                                                                                                                                                                                                                                                                                                              21 APASSSTKETQQQLEQLLLDLRLLLNGVNN 50
                                                                                                                                                                                                                                                                                         1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
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TISSUE=Blood;
Markus S., Groene A., Baumgaertner W.;
                                 4 KI
150 F
17653 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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   111 1
3
150 1
154 AA;
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                              CONFLICT
CONFLICT
SEQUENCE
   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9XT83
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Q9XT83
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STRAIN=Beagle; TISSUB=Spleen;
MEDLINE=95347614; PubMed=7622066; DOI=10.1016/0378-1119(95)00078-K;
MEDLINE=95347614; PubMed=7622066; DOI=10.1016/0378-1119(95)00078-K;
Knapp D.W., Williams J.S., Andrisani O.M.;
"Cloning of the canine interleukin-2-encoding cDNA.";
Gene 159:281-282(1995).
-!- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine—activated killer cells, matural killer cells, and glioma cells.
-!- SIBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96016696; PubMed=8571541; DOI=10.1016/0165-2427(94)05400-M; Somberg R.L., Pullen R.P., Casal M.L., Patterson D.F., Felsburg P.J. Henthorn P.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A single nucleotide insertion in the canine interleukin-2 receptor gamma chain results in X-linked severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Pissipedia, Canidae, Canis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112_CANFA STANDARD; PRT; 155 AA. 029416; 028249; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) 11-JUL-1998 (Rel. 24, Last annotation update) 11-JUL-1998 (Rel. 27, Carl growth factor) (TCGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=XBRED21/12/93; TISSUB=Lymph node;
MEDLINE=95337423; PubMed=7612930;
Dunham S.P., Argyle D.J., Onlons D.E.;
"The isolation and sequence of canine interleukin-2.";
DNA Seq. 5:177-180(1995).
                                                                  GO; GO: 0005576; C: extracellular; IEA.
GO; GO: 0005134; F: interleukin-2 receptor binding; IEA.
GO; GO: 0005134; F: interleukin-2 receptor binding; IEA.
GO; GO: 00059576; P: immune response; IEA.
InterPro; IPR009079; J. halix cytokine.
InterPro; IPR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 AA; 7389 MW; 22A893F79DA2AE47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 107.5; DB 2
Pred. No. 1.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vet. Immunol. Immunopathol. 47:203-213(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.1%; Scor.
71.0%; Pred. No. 1...
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 APITSSSTKETEQOMEQLLLDLOLLLNGVNN 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AP-TSSSTKKTQLQLEHLLLDLQMILNGINN 30
EMBL; AF333117; AAK01437.1; -. HSSP; P60568; 1IRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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1;

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Gaps
                                                                                                                                                                                                                                                                                                                                           Schountz T., Buniger A., Davenport B., Hegg T.; "Cloning of deer mouse IL-2, IL-12 p35, IL-21, GM-CSF, CCL3 and CCL4 cDNAs.";
                                                                                                                                                                                                                             Peromyscus maniculatus (Deer mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
NCBI_TaxID=9986;
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15-JUL-1999 (Rel. 38, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TGGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AY247766; AAP0449-1; ...

EMBL; AY247766; AAP0449-1; ...

EMBL; P60568; 11RL.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:000514; F:interleukin-2 receptor binding; IEA.

GO; GO:0006955; P:immune response; IEA.

InterPro; IPR009079; 4 helix_cytokine.

InterPro; IPR009079; 1 Herieukin-2.

Pfam; PF00715; IL2; 1.

PRINTS; PR00265; INTERLEUKIN2.

ProDom; PD003649; Interleukin-2; 1.

ProDom; PR00189; IL2; 1.

PROSITE; S00424; INTERLEUKIN 2; 1.

NOW TER 152, 152
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER 152 152 - SEQÜENCE 152 AA; 17095 MW; 798D13514AD0CC93 CRC64;
                                                                                                                                              (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.8%; Score 107; DB 2; 70.0%; Pred. No. 5.9e-08;
                                                                                                                     152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
      3 ISSSTKKTQLQLEHLLLDLQMILNGINN 30
                     21 APTSSSTKETQQHLEQLLMDLEVLLKGINN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                     PRT;
                                                                                                                                                                                                Interleukin-2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 70.0 nes 21; Conservative
                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           NCBI_TaxID=10042;
                                                                                                                                                 01-JUN-2003
                                                                                                                                                                01-JUN-2003
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.2 RABIT
07.7620;
                                                                                                                                                                                                                 Name=112;
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                                                                                                                   Q80XG3
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IL2_RABIT
ID IL2_R
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      and for commercial
   loved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                          (By similarity) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canis ramiliaris vosy.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.8%; Score 107; DB 2; Length 79
Best Local Similarity 71.4%; Pred. No. 2.8e-08;
Matches 20; Conservative 6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                       By similarity.
Interleukin-2.
O-linked (GalNAc. ..) (By in N-linked (GlonAc. ..) (Pot. By similarity.
M -> I (in Ref. 3).
Q -> R (in Ref. 3).
F -> Y (in Ref. 3).
L -> M (in Ref. 3).
L -> M (in Ref. 3).
M, Dl23B486B7F4ACID CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF091131, AAD46989.1;
HSSP; P60568; 11RL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR009079; J. halix cytokine.
InterPro; IPR000779; Interleukin-2.
Pfam; PR00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
SMART; SM00189; IL2; 1.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 107.5; DB 1
Pred. No. 5.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 AA.
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AP-TSSSTKKTQLQLEHLLLDLQMILNGINN 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 APITSSTKETEQOMEQLLLDLOLLLENGVNN 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
               entities requires a license agreement ( or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                         17668 MW;
                                                            EMBL; D30710; BAA06378.1; -. EMBL; U28141; AAA68969.1; -. EMBL; U11689; AAA75360.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.1%;
71.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 71.0°
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interleukin-2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                      154 1
155 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 AA;
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CARBOHYD
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SEQUENCE
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CONFLICT
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Best Local Similarity
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NCBI_TaxID=10036;
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                                      Query Match
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                                                                                                Matches
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070329
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Interleukin-2.
Interleukin-2.
Interdeukin-2.
N-linked (GalNAc. . .) (By similarity).
N-linked (GlCNAc. . .) (Potential).
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"The complete CDNA sequences of IL-2, IL-4, IL-6 AND IL-10 from the Buropean rabbit (Oryctolagus cuniculus).";
EMBL; AF169168; AAF86652.1;
BMSL; AF169168; AAF86652.1;
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:000595; P:immune response; IEA.
InterPro; IPR000979; 4 helix cytokine.
InterPro; IPR000979; Interleukin-2.
immune response. Can stimulate B cells, monocytes, lymphokine-activated Killer cells, natural Killer cells, and glioma cells. SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to the IL-2 family.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
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TISSUE=Spleen;
MEDLINE=20304414; PubMed=10843729; DOI=10.1006/cyto.1999.0658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 107; DB 1; Length 15
Pred. No. 5.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00715; IL2; 1.
ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
SROGA24; INTERLEUKIN 2; 1.
SEQUENCE 133 AA; 14748 MW; 0D54758C190B5655 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / similarity.
8173536B2DDD8B86 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AF068057; AAC23838.1; -. HSSP; P01585; IM4A.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interleukin 2 variant IL2delta2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.8%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 70.v.
Local 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 AA;
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Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
"Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
analysis of cytokine mRNA expression in experimental visceral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Darmell M.R., Pletneva L.M., Langley R.J., Blanco J.C., Prince G.A.; Submitted (ULL-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AF398549; AAK44012.1; -.
HSSP; P60568; 1IRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
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Mesocriceus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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                       Score 106; DB 2; Length 133;
Pred. No. 7.2e-08;
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Local Similarity 73.3%; Pred. No. 8.6e-08;
Les 22; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 155 AA: 17627 MW; ACADEA865E993291 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005576; C:extracellular; IEA.
GO; GO:000514; P:interleukin-2 receptor binding; IEA.
GO; GO:0005955; P:immune response; IEA.
Pfam; PF00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
PRODO3649; ILZ; 1.
SMART; SM00189; IL2; 1.
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
72.1%; Sco...
72.4%; Pred. No. ...
5; Mismatches
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                                                                                                                                      1 APTSSSTKKTQLQLEHLLLDLQMILNGIN 29
                                                                                                                                                                   21 APTSSSTKETQEQLDQLLLDLQVLLKGVN 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sigmodon hispidus (Hispid cotton rat).
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EMBL, AF046212; AAC40097.1; --
HSSP; P60568; 1IRL.
                                                                              21; Conservative
                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenetics 30:145-147(1989).

-!- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine activated killer cells, natural killer cells, and glioma cells.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89339608; PubMed=2788130;
McKnight A.J., Mason D.W., Barclay A.N.;
"Sequence of rat interlin 2 and anomalous binding of a mouse
interleukin 2 cDNA probe to rat MRC class II-associated invariant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
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01-AUG-1990 (Rel. 15, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                    138 AA; 15739 MW; 351032995B670779 CRC64;
GO; GO:0005134; F:interleukin-2 receptor binding; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 70.1%; Score 103; DB 2; L. Best Local Similarity 73.3%; Pred. No. 2.1e-07; Matches 22; Conservative 2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
                           GO; GO:0006955; P:immune response; IEP.
InterPro; IRR009079; 4 helix cytokine.
InterPro; IPR000779; Interleukin-2.
Pfam; PP00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
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RGDJ, 62047, II.12.

InterPro; IPR009079; 4 helix cytokine.

InterPro; IPR000779; Interleukin-2.

Pfam; PR0015; IL2, IL.

PRINTS; PR00265; INTERLEUKIN2.

ProDom; PD003649; Interleukin-2; 1.
                                                                                                                                                                                                                                                                  PROSITE; PS00424; INTERLEUKIN_2; 1.
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SEQUENCE
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goodall J.C., Emery D.C., Bailey M., English L.S., Hall L.;
"CDNA cloning of porcine interleukin 2 by polymerase chain reaction.";
Biochim. Biophys. Acta 1089:257-258(1991).
                                                                                                                                                                                   Gaps
Interleukin-2.
O-linked (dalNac. . .) (By similarity).
ps similarity.
67A8554A73BF30A0 CRC64;
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MEDLINE=91274360; PubMed=2054386; DOI=10.1016/0167-4781(91)90019-I;
MEDLINE=91274360; PubMed=2054386; DOI=10.1016/0167-4781(91)90019-I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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InterPro; IPR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
PRODOM; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
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01-AUG-1992 (Rel. 23, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TGGF).
                                                                                                                           Length 155;
                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lefevre F.;
Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                              Score 97; DB 1;
Pred. No. 2e-06;
4; Mismatches
                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                 1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
                                                                                                                                                                                                                                                              21 APTSSPAKETQQHLEQLLLDLQVLLRGIDN
                                                                        17632 MW;
                                                                                                                              66.0%;
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PIR, S16241, S16241.
HSSP, P01585, 1M49.
                                                                                                                                                                              20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                        155 AA;
                                                                                                                              Query Match
Best Local Similarity
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Best Local Similarity
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P37997;
                                                                                                                                           Q865X2
                                                                                                           RESULT 35
Q865X2
                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Spieen;
MEDLINE-94174702; PubMed=8128610; DOI=10.1016/0165-2427(94)90015-9;
Mai Z., Kousoulas K.G., Horobov D.W., Klei T.R.;
"Cross-species PCR cloning of gerbil (Meriones unguiculatus)
interleukin-2 cDNA and its expression in COS-7 cells.";
Vet. Immunol. Immunopathol. 40:63-71(1994).
-! FUNCTION: Produced by T-cells in response to antigenic or
mitogenic stimulation, this protein is required for T-cell
proliferation and other activities crucial to regulation of the
immune response. Can stimulate B cells, monocytes, lymphokine-
activated killer cells, natural killer cells, and glioma cells.
                                                                                                                              Gaps
              By similarity.
Interleukin-2.
O-linked (GalNAc. . .) (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
                                                                                                                              ö
                                                                                                                                                                                                                                                                              01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
                                                                                                65.3%; Score 96; DB 1; Length 154; ilarity 66.7%; Pred. No. 2.8e-06; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                      Meriones unguiculatus (Mongolian jird) (Mongolian gerbil)
                                                        By similarity.
F3B95E43D4A3D3E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
: DOF74AA1A381CDDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interleukin-2.
O-linked (GalNAc.
                                                                                                                                                                                                                                                        155 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the IL-2 family.
                                                                                                             Pred. No. 2.86
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity.
                                                                                                                                                       1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                       21 APTSSSTKNTKKQLEPLLLDLQLLLKEVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, PO1588; 1M49.
InterPro; IPR009079; 4_helix_cytokine.
InterPro; IRR0000779; Interleukin-2.
Pfam; PF00715; ILZ; 1.
PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
                                                                                                                                                                                                                                                       PRT;
             1 20 By
21 154 Int
23 23 0-1
78 126 By
154 AA; 17401 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17602 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X68779; CAA48679.1; -. PIR; S33509; S33509.
                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
155
23
                                                                                                             Local Similarity
les 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10047;
                                                                                                                                                                                                                                                      IL2 MERUN
                                                                                                                                                                                                                                                                                                                                          Name=IL2;
                                                       DISULFID
                                          CARBOHYD
                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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SIGNAL
T-cell.
SIGNAL
                              CHAIN
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Matches
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IL2 MERUN
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DB 1; Length 155;

64.6%; Score 95;

Query Match

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                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Raadan O., Lee S.-., Yoshida R., Chang K.-., Ohashi K., Sugimoto C.,
Onuma M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94160538; PubMed=8116217; DOI=10.1016/0165-2427(93)90070-K; Vandergrifft E.V., Horohov D.W.; "Molecular cloning and expression of equine interleukin 2."; Vet. Immunol. Immunopathol. 39:395-406(1993).
                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi,
Mammalia, Butheria, Cetartiodactyla, Tylopoda, Camelidae, Lama.
NCBI_TaxID=9844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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01-NOV-1995 (Rel. 32, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TGGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.3%; Score 93; DB 2; Length 154
66.7%; Pred. No. 7.9e-06;
iive 3; Mismatches 7; Indels
                           Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB107651; BAC75388.1; -.
HSSP; P60568; 1IRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM0189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 154 AA; 17652 MW; 8020EC8DDB7BBA38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO: GO:0005576; C:extracellular; IEA.
GO: GO:000514; F:interleukin-2 receptor binding; IEA.
GO: GO:0005134; F:interleukin-2 receptor binding; IEA.
GO: GO:0006955; P:immune response; IEA.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR00779; Interleukin-2.
PATMIN; PR00265; INTERLEUKIN2.
PRODM; PD003649; Interleukin-2; 1.
                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                         ..
..
   4e-06;
                                                                                                                                                                                                   154 AA
66.7%; Prec. ....
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                                                                                     21 APTSSPAKEAQYLEQLLLDLQQLLRGINN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 APTLSSTKOTKKOLEPLLLDLOFLLKEVNN 50
                                                               1 APTSSSTKKTQLQLEHLLLDLQMILNGINN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                       20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 66.7 tes 20; Conservative
                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                   Lama glama (Llama).
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                 Interleukin 2.
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90.5%;

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19; Conservative
      Best Local Similarity
                                                                                                                                                                                                         (Fragment).
Name=IL2;
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SEQUENCE
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                 Matches
                                                                                                      RESULT 38
IL2 ORCOR
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                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                             (By similarity).
(Potential).
mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.
-!- SUBCELJULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                    EMBL; L06009; AAA20134.1; --
BMBL; X69393; CAA49190.1; --
PIR; S31391; S31391.
HSP; P01585; 1M47.
InterPro; IPR009079; 4_helix_cytokine.
InterPro; IPR00179; Interleukin-2.
Pfam; PF00715; IL2; I.
PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
CYtokine; Glycoprotein; Growth factor; Immune response; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93289963; PubMed=8512072; DOI=10.1006/abio.1993.1209; Mullner S., Karbe-Thonges B., Tripier D.; "Charge heterogeneity of insulin fuelon proteins expressed in Bscherichia coli is not due tro proteolytic degradation."; Anal. Biochem. 210.366-373(1993).
SEQUENCE 23 AA; 2637 MW; 40B64C6875CE021F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 92; DB 1; Length 149;
Pred. No. 1.1e-05;
8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     R -> K (in Ref. 2).
S -> A (in Ref. 2).
I -> M (in Ref. 2).
N -> D (in Ref. 2).
E -> G (in Ref. 2).
E -> G (in Ref. 2).
I -> F (in Ref. 2).
OSIBBBC47A0114FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                             By similarity.
O-linked (GalNAc. .) (E
N-linked (GloNAc. .) (E
R -> K (in Ref. 2).
S -> A (in Ref. 2).
I -> M (in Ref. 2).
I -> M (in Ref. 2).
I -> F (in Ref. 2).
I -> K (in Ref. 2).
I -> K (in Ref. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UCF5;
Q9UCMXY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 AA
                                                                                                                                                                                                                                                                                                                                                        By similarity.
Interleukin-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 APTSSSKRETQQQLKQLQMDLKLLLEGVNN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17086 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 56.7%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interleukin 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 1
148 1
149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                              T-cell.
                                                                                                                                                                                                                                                                                                                                                        SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 37
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61.9%; Score 91; DB 2; Length 23;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mar. Mamm. Sci. 14:531-543(1998).
-!- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Cetacea, Odontoceti, Delphinidae,
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ness T.L., Bradley W.G., Reynolds J.E. III, Roess W.B.; "Isolation and expression of the interleukin-2 gene from the killer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .) (By similarity)
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                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 152;
                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 20 By similarity.
21 >152 Interleukin-2.
23 23 0-linked (GalNac. ..) (By 78 126 By similarity.
152 152 17424 MW; 308F91821ECCE764 CRC64;
Pred. No. 1.9e-06;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 88; DB 1; Pred. No. 4.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                         152 AA
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                                                                                                                                                                                                                                                         PRT;
                                                                            3 TSSSTKKTQLQLEHLLLDLQM 23
                                                                                                              3 TSXSTKKTQLQLEHLXLDLQM 23
                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF009570; AAD01426.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Orcinus orca (Killer whale).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.98;
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Matches 18; Conservative
                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         whale, Orcinus orca.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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MEDIJNE=99221046; PubMed=10206205; DOI=10.1016/S0165-2427(99)00009-4;
St-Laurent G., Beliveau C., Archambault D.;
"Molecular cloning and phylogenetic analysis of beluga whale
(Delphinapterus leucas) and grey seal (Halichoerus grypus) interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                               071V48;
051V48;
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
105-JUL-2004 (TrEMBLrel. 27, Last annotation update)
105-JUL-2004 (Tremment).
Homo sepiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Interleukin 2.
Delphinapterus leucas (Beluga whale).
Bukaryota; Metascas; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Cetacea; Odontoceti;
Monodontidae; Delphinapterus.
[11]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO: 0005576; C: extracellular; IEA.
GO; GO: 000514; F: interleukin-2 receptor binding; IEA.
GO; GO: 0006515; F: immune response; IEA.
GO; GO: 000655; P: immune response; IEA.
InterPro; IPR000709; Interleukin-2.
InterPro; IPR00779; Interleukin-2.
InterPro; IPR0055; INTERLEUKIN2.
IPRODm; PD003649; Interleukin-2; 1.
IPRNTS; PR00365; INTERLEUKIN2.
IPROSITE; PS00424; INTERLEUKIN 2; 1.
IPROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 154 AA; 17652 MW; 4288D3D41D04F172 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 59.2%; Score 87; DB 2; Length 38; Best Local Similarity 100.0%; Pred. No. 1.3e-05; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                  Turner D.M., Sinnott P.J., Hutchinson I.V., Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF031845; AAB86861.1; -
                                                                                                                                                                                                                                                                                                       GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
DicerPro; IPR000779; Interleukin-2.
PF00715; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                               Probom; P0003649; Interleukin-2; 1.
NON TER 38 38
SEQUENCE 38 AA; 4192 MW; 8DE4AE5344C2CBA3 CRC64;
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EMBL; AF072870; AAD40847.1;
HSSP; P60568; IIRL.
                                     38 AA.
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                                  PRELIMINARY;
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RESULT 39
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                    GenCore version 5.1.6
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Database

Result

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3-isopropylmalate
phenylalanyl-tRNA
hypothetical cell
coll intron protei
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Gypol3.3 proteinGypothetical protei
hypothetical protei
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probable integral
hypothetical prote

two-component hybr cinnamyl-alcohol d cinnamyl-alcohol d

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multidrug efflux p
myelin transcripti
transcription fact

pol polyprotein f22b7.5 protein

zinc finger protei exodeoxyribonuclea hypothetical prote hypothetical prote

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F64145 H64307

AB1367 AC1736 GNLJG4 T11685

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## ALIGNMENTS

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A; Molecule type: mRNA
A; Residues: 1-153 < MAE.
A; Cross-reterences: GB-J00264; NID:g186294; PIDN:AAD48509.1; PID:g5729676
A; Experimental source: tonsillar mononuclear cells
R; Devos, R.; Plaetinck, G.; Cheroutre, H.; Simons, G.; Degrave, W.; Tavernier, J.; Remau
Nucleic Acids Res. 11, 4307-4323, 1993
A; Title: Molecular cloning of human interleukin 2 cDNA and its expression in Escherichia
A; Reference number: A93478; MUID:83246551; PMID:6306584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781
A,Experimental source: splenocytes
R;Eizenberg, O.; Faber-Elman, A.; Lotan, M.; Schwartz, M.
J. Neurochem. 64, 1928-1936, 1995
A;Title: Interleukin-2 transcripts in human and rodent brains: possible expression by as A;Reference number: I56518; MUID:95239150; PMID:7722480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M33199; NID:g186296; PIDN:AAA59139.1; PID:g553508
R;Siebenlist, U.; Durand, D.B.; Bressler, P.; Holbrook, N.J.; Norris, C.A.; Kamoun, M.;
Mc). Cell. Biol. 6, 3042-3049, 1986
A;Title: Promoter region of interleukin-2 gene undergoes chromatin structure changes and A;Reference number: I57603; MUID:87064618; PMID:3491296
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A;Cross-references: GB:M22005; NID:g186300; PIDN:AAA59140.1; PID:g386818
A;Note: mutation of Phe-42 to Ala reduced binding to the IL-2 receptor 5-10 fold without
                                                           chromosomal bre
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781
A;Experimental source: leukemic T-cell line, Jurkat-111, cloned from Jurkat-FHCRC
R;Maeda, S.; Nishino, N.; Obaru, K.; Mita, S.; Nomiyama, H.; Shimada, K.; Fujimoto, K.;
Biochem. Biophys. Res. Comuun. 115, 1040-1047, 1983
A;Title: Cloning of interleukin 2 mRNAs from human tonsils.
A;Reference number: A90113; MUID:84023840; PMID:6312994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Readidues: 5-7,7F',9-17,7P',19-32,7X',34-45,7X',47-143 <RES>
A;Cross-references: GB:377835; NID:g999001; PIDN:AAD14264.1; PID:g4261964
A;Cross-references: GB:377835; NID:g999001; PIDN:AAD14264.1; PID:g4261964
B;Nishino, N.; Obaru, K.; Maeda, S.; Shimada, K.; Onoue, K.
Biomed. Res. 6, 197-205, 1985
A;Title: Organization of the DNA regions flanking the human interleukin 2 gene.
A,Cross-references: EMBL:Z14955
A,Note: this sequence is shown from the beginning of the fragment to the chrom A,Note: this sequence is shown from the beginning of the fragment to the chrom R; Taniguchi, T.; Matsui, H.; Fujita, T.; Takaoka, C.; Kashima, N.; Yoshimoto, Nature 302, 305-310, 1983
A; Title: Structure and expression of a cloned cDNA for human interleukin-2.
A; Reference number: A93297; MUID:83167472; PMID:6403867
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A;Cross-references: GB:M13879; NID:g186305; PIDN:AAA59141.1; PID:g553509
A;Cross-references: GB:M13879; NID:g186305; PIDN:AAA59141.1; PID:g553509
R;Weiri, M.P.; Chaplin, M.A.; Wallace, D.M.; Dykes, C.W.; Hobden, A.N.
Biochemistry 27, 6881-6893. 1988
A;Title: Structure-activity relationships of recombinant human interleukin A;Reference number: 152401; MUID:89062420; PMID:3264184
A;Contents: recombinant IL-2 and mutants expressed in B. coli
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A;Residues: 1-152 <EIZ>
A;Cross-references: GB:S77834; NID:g999000
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A;Molecule type: DNA
A;Residues: 1-68 <RE2>
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A;Accession: 152528
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A;Residues: 1-153 <DEV>
                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-153 < TAN>
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A; Molecule type: mR
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Natherate names: III-2; T-cell growth factor
C;Species: Howo sapiens (man)
C;Date: 11-Aug-1933 #sequence revision 11-Aug-1933 #text_change 09-Jul-2004
C;Accession: A01849; A2192; A2093; S31209; A33297; A90Il3; A93478; IS6518; I73624; IS2
R;Hobbrook, N.J.; Lieber, M.; Crabtree, G3
R;Hobbrook, N.J.; Lieber, M.; Crabtree, G4
A;Title: DNA sequence of the 5' flanking region of the human interleukin 2 gene: homolog
A;Rceference number: A93524; MUID:84247353; PMID:6330695
A;Cross-references C4
A;Cross-references C5
A;Accession: A1192
A;Title: Structure of the human interleukin 2 gene.
A;Reference number: A2192; MUID:84170243; PMID:6324170
A;Reference number: A2192; MUID:84170243; PMID:6324170
A;Reference number: A2192; MUID:84170243; PMID:84080991; PID:85728676
B;Hobbrook, N.J.; Smith, K.A.; Fornace Jr. A.J.; Comeau, C.M.; Wiskocil, R.L.; Crabtree
A;Reference number: A20961; MUID:84170356; PMID:660879
A;Accession: A20961
A;Accession: A20961
A;Accession: A20961
A;Accession: A20961
A;Readules: 1-153 -4HO2
A;R
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A;Thtle: A viral long terminal repeat in the interleukin 2 gene of a cell line that cons A; Reference number: A94067; MUID:86042650; PMID:3877307

A;Reference number: A94067; MUID:86042650; PMID:3877307

A;Residues: 1-153 cCHE>
A;Residues: 1-153 cCHE>
A;Residues: 1-153 cCHE>
A;Residues: U.S.A. CHE>
A;Residues: U.S.A. CHE>
A;Residues: U.S.A. CHE>
A;Residues: U.S.A. CHE>
A;Roserimental source: leukemia cell line MLA 144; ATCC TIB 201
A;Rote: the integration of a retrovirus sequence containing a 5' LTR into the 3' noncodi C;Superfamily: interleukin-2
C;Reywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell F;-20/Domain: signal sequence #status predicted <SIG>
F;21-153/Product: interleukin-2 #status predicted <SIG>
F;21-153/Product: interleukin-2 #status predicted <IL2>
F;23/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;78-125/Disulfide bonds: #status predicted
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                                                                                                                                               ...celleuxin-2 precursor - common gibbon
|Alternate names: IL-2; T-cell growth factor
|Species: Hylobates lar (common gibbon, white-handed gibbon)
|Bate: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
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100.0%; Pred. No. 2.3e-14;
ive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 30; Conservative
                                                                                                                                                                                       interleukin-2 precursor
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A; Reference number: A34463; MUID: 90008901; PMID: 2793860

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N.Alternate names: IL-2; T-cill growth factor C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Date: 26-Apr-1989 #sequence_revision 26-Apr-1989 #text_change 09-Jul-2004 C;Date: 26-Apr-1989 #sequence_revision 26-Apr-1989 #text_change 09-Jul-2004 C;Date: 26-Apr-1980; A.J.; Mason, D.W.; Barclay, A.N. Immunogenetics 30, 145-147, 1989 A.P. Immunogenetics 30, 145-147, 1989 A.P. Immunogenetics of rat interleukin 2 and anomalous binding of a mouse interleukin 2 cl A;Reference unmber: A45882 MUID:89339608; PMID:2788130 A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P17108; GB:M22899; NID:g204909; PIDN:AAA41427.1; PID:g20491C
C;Superfamily: interleukin-2
C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S33509
R;Mai, Z.; Klei, T.; Horohov, D.
submitted to the EMBL Data Library, October 1992
A;Description: Cross-species FCR cloning of Jird (Meriones unguiculatus) interleukin-2 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RiLefevre, F. submitted to the EMBL Data Library, March 1991
A;Description: Molecular cloning of porcine interleukin 2 cDNA by the polymerase chain A;Reference number: $15473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: UNIPROT: P26891; EMBL: X56750; NID: g1991; PIDN: CAA40071.1; PID: g1992
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N;Alternate names: IL-2; T-cell growth factor
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S16241; S15473
R;Goodall, J.C.; Emery, D.C.; Bailey, M.; English, L.S.; Hall, L.
Biochim. Biophys. Acta 1089, 257-258, 1991
Biochim. Elophys. Acta 1089, 257-258, 1991
A;Title: cDNA cloning of porcine interleukin 2 by polymerase chain reaction.
A;Reference number: S16241; MUID:91274360; PMID:2054386
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C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-154/Product: interleukin-2 #status predicted <MAT>
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C;Superfamily: interleukin-2
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8.4e-07;
6;
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Pred. No. 6e-07;
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Pred. No. 8.4e
4; Mismatches
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Best Local Similarity 66.7
Matches 20; Conservative
                                        interleukin-2 precursor
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Matches 20; Conserv
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A; Residues: 1-155 <MCK>
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A; Residues: 1-154 <GOO>
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R;Robb, R.J.; Kutny, R.M.; Panico, M.; Morris, H.R.; Chowdhry, V.

Proc. Natl. Acad. Sci. U.S.A. 81, 6486-6490, 1984
A;Title: Amino acid sequence and post-translational modification of human interleukin 2.
A;Reference number: A94009; MUID:85038540; PMID:6333684
A;Accession: A94009
A;Accession of human interleukin-2 is primarily due to differences in glycosyl n in lacking 21-Ala (FT-IL2-B) and 22-Pro (FT-IL2-B)
B;Conradt, H.S.; Nimtz, M.; Dittmar, K.E.J.; Lindenmaier, W.; Hoppe, J.; Hauser, H.
J. Biol. Chem. 264, 17368-17373, 1989
A;Title: Expression of human interleukin-2 in recombinant baby hamster kidney, Ltk-, and de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Accession: A34463
A,Molecule type: protein
A,Molecule type: protein
A,Rosidues: 21-35 <CON>
A;Note: the O-linked glycosylation site in recombinant material matched that from human
A;Note: the O-linked glycosylation site in recombinant material matched that from human
A;Note: the O-linked glycosylation site in recombinant H.S.

Bur. J. Biochem. 215, 189-197, 1993
A;Title: Biosynthesis and secretion of human interleukin 2 glycoproteins variants from b
A;Reference number: S34052; MUID:9334543; PMID:8344280
C;Genetics: annotation; glycosylation of variant forms expressed in insect cells
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Pred. No. 1.8e-09;
5; Mismatches 3; Indels
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1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30

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Local Similarity 100. nes 30; Conservative

21 APTSSSTKKTQLQLEHLLLDLQMILNGINN

interleukin 2 precursor - cat

RESULT

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Query Match
Best Local Similarity 73.3%;
Matches 22; Conservative

Matches

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A;Status: preliminary
A;Molecule type: mENA
A;Residues: 1-152 ARIM-
A;Cross.references: UNIPROT:P36835; EMBL:X76063; NID:g416002; PIDN:CAA53664.1; PID:g4160.
C;Superfamily: interleukin-2
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Nucleic Acids Res. 18, 7175, 1990
A,Title: The molecular cloning of ovine interleukin 2 gene by the polymerase chain react A;Reference number: S13102; MUID:91088336; PMID:2263496
                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Capra agggrus hircus (domestic goat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S38662
R;Rimetad, E.
submitted to the EMBL Data Library, November 1993
A;Bescription: The molecular cloning and expression of caprine interleukin 2.
A;Reference number: S38662
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C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S11488; S13102; S15517
R;Goodall, J.C.; Emery, D.C.; Perry, A.C.F.; English, L.S.; Hall, L.
Nucleic Acids Res. 18, S883, 1990
A;Title: cDNA cloning of ovine interleukin 2 by PCR.
A;Reference number: S11488; MUID:91016933; PMID:2216781
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A; Residues: 1-5,'L',7-155 <SEO>
A; Cross-references: EMBL:X55641; NID:g1810; PIDN:CAA39165.1; PID:g1811
R; Bujdoso, R.; Williamson, M.L.; Sargan, D.R.; Hein, W.H.; McConnell, I.
submitted to the EMBL Data Library, April 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 155;
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Pred. No. 0.00028;
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No. 0.00028;
                                                                                                                         21 APTSSSTGNTMKEVKSLLLDLQLLLEKVKN 50
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                                                               1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
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A;Residues: 21-153 <BUJ>
A;Cross-references: EMBL:X60148
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Best Local Similarity 53.3
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: interleukin-2
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A; Accession: $15517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Status: preliminary
A Molecule type: mRNA
A Residues: 1-155 <GOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                       interleukin-2 - goat
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C;Species: Bos primigenius taurus (cattle)
C;Stecession: 145913; S21470; S20761
R;Cerretti, D.P.; McKereghan, K.; Larsen, A.; Cantrell, M.A.; Anderson, D.; Gillis, S.;
Proc. Natl. Acad. Sci. U.S.A. 83, 323-3227, 1986
A;Title: Ciloning, sequence, and expression of bovine interleukin 2.
A;Reference number: 145913; MUID:86205869; PMID:3517864
A;Reference number: 145913; MUID:86205869; PMID:3517864
A;Reducle type: mRNA
A;Residues: 1-155 «CER»
A;Cross-references: UNIPROT:POSO16; GB:M12791; NID:g163204; PIDN:AAA30586.1; PID:g163205
R;Anikeeva, N.N.; Vinogradova, T.V.; Votoshin, O.N.
submitted to the EMBL Data Library, December 1989
A;Reference number: S21470
A;Molecule type: DNA
A;Residues: 1-22 «AN2>
A;Cross-references: EMBL:X17201; NID:g452; PIDN:CAA35062.1; PID:g453
C;Genetics:
C;Superfemily: interleukin-2
C;Superfemily: interleukin-2
C;Superfemily: interleukin-2
C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell
                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 «MAI>
A;Cross-references: UNIPROT:Q08081; EMBL:X68779; NID:g577588; PIDN:CAA48679.1; PID:g3116
C;Superfamily: interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              incerleukin-2 precursor - horse
G/species: Equue caballus (domestic horse)
G/species: Equue caballus (domestic horse)
G/scession: 831391
G/Accession: 831391
A/Ravernor, A.S.; Butcher, G.W.
submitted to the EMBL Data Library, November 1992
A/Reference number: 831391
A/Accession: 831391
A/Accession: 831391
A/Accession: B31391

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:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine;
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                                                                                                                                                                                                                                                                                                                                                                                  tch 64.6%; Score 95; DB 2; Length 155; al Similarity 66.7%; Pred. No. 1.2e-06; 20; Conservative 2; Mismatches p. The construction of the construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 62.6%; Score 92; DB 2; Length 149; Best Local Similarity 56.7%; Pred. No. 3.2e-06; Matches 17; Conservative 8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 79; DB 2; Length 155;
Pred. No. 0.00028;
5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 APTSSPAKEAQYLEQLLLDLQQLLRGINN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 APTSSSTKKTQLQLEHLLLDLQMILNGINN 30
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Best Local Similarity 53.3%;
Matches 16; Conservative
Reference number: S33509
Accession: S33509
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Best Local Similarity
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A; Molecule type: mRNA
A; Residues: 1-169 < YOK>
A; Residues: 1-169 < YOK>
A; Crose-references: GB: K02292; NID:g198330; PIDN:AAA39289.1; PID:g309404
B; Kashima, N.; Nish: Takaoka, C.; Fujita, T.; Taki, S.; Yamada, G.; Hamuro, J.; Tanigucl
Nature 313, 402-404, 1985
A; Title: Olique structure of murine interleukin-2 as deduced from cloned cDNAs.
A; Reference number: 148597; MUID:85111148; PMID:2578624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X01772; GB:K02797; NID:g52663; PIDN:CAA25909.1; PID:g758159 C;Comment: Produced by T-cells in response to antigenic or mitogenic stimulation, this F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q08867; GB:L07575; NID:g349515; PIDN:AAA39327.1; PID:g349516
C;Genetics:
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C;Species: O2-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C;Accession: 154512
R;Accession: 154512
Immunogenetics 38, 300-303, 1993
A;Fitle: Existence of at least five interleukin-2 molecules in different mouse strains.
A;Reference number: 154512; MUID:93307791; PMID:8319981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell F:1-20/Domain: signal sequence #status predicted <SIG> F:21-169/Product: interleukin-2 #status predicted <MAT> F:23/Bainding site: carbohydrate (Thr) (covalent) #status predicted F:92-140/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus spretus (western wild mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I68870
R;Matessarz, F: Alcina, A.; Pellicer, A.
Immunogenetics 38, 300-303, 1993
A;Title: Existence of at least five interleukin-2 molecules in different mouse strains.
A;Reference number: 154512; MUID:93307791; PMID:8319981
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A; Reference number: A94064; MUID:85113172; PMID:3918306
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A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 43.5%; Score 64; DB 1; Best Local Similarity 38.6%; Pred. No. 0.052; Matches 17; Conservative 6; Mismatches
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45.5%; Pred. No. 0.075;
iive 6; Mismatches
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interleukin 2 - mouse (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 63/3; 83/3; 132/3
C;Superfamily: interleukin-2
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C;Superfamily: interleukin-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-169 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-60 <RES>
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Algebrance number: 1-169 <-TOD>

Algebrance number: 1-169 <-TOD>

Algebrance number: 237205, MUD: 93041941; PMD: 1420317

Algebrance number: 327205, MUD: 93041941; PMD: 1420317

Algebrance number: 327205

Algebrance number: 328162; MUD: 94004970; PMID: 8401590

Algebrance number: 336162; MUD: 94004970; PMID: 8401590

Algebrance number: 336162; MUD: 94004970; PMID: 8401590

Algebrance number: 336162; MUD: 94004970; PMID: 8401590

Algebrance number: 326162; MUD: 94004970; PMID: 8401590

Algebrance number: 326162; MUD: 94004970; PMID: 8401590

Algebrance number: 326162; MUD: 94004970; PMID: 8401590

Algebrance number: SMBL: X73040

Algebrance number: SMBL: X73040

Algebrance number: SMBL: X73040
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A; Molecule type: DNA
A; Residues: 1-169 < FUS.
A; Reference uniber: G; Devos, R; Plaetinck, G; Remaut, E; Tavernier, J; Fiers, M
A; Title: Cloning and structure of a mouse interleukin-2 chromosomal gene.
A; Reference number: A54490; MUID:86118396; PMID:3003564
A; Accession: A54490
A; A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-169 < DEGA
A; Aresidues: 1-169 < DEGA
A; Aresidues: 1-169 < DEGA
A; Aresidues: 1-169 < DEGA
A; Cross references: GB:M16760
A; Title: Use of a cDNA expression vector for isolation of mouse interleukin 2 cDNA clone
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N.Alternate names: IL-2; T-cell growth factor (TCGF)
S.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: 30-Jun-1987 #sequence revision 30-Jun-1987 #text change 09-Jul-2004
C.Accession: A93550; A54490; Ā94064; I48597; A01850; I84713
S.Fune, A.; Puljita, T.; Yasumiteu, H.; Kashima, N.; Hasegawa, K.; Taniguchi, T.
Nucleic Acids Res. 12, 9323-9331, 1984
A.Title: Organization and structure of the mouse interleukin-2 gene.
A.Reference number: A93550; MUID:85087940; PMID:6240025
                                                                                                                                                                        Species: Mus musculus (house mouse)
Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
Accession: S37289; S27205; S36162; S24936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 0.0094;
6; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                      R;Todd, J.A. submitted to the EMBL Data Library, April 1993
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1. Similarity 47.2%;
17; Conservative
                                                                                                                                             interleukin-2 precursor - mouse
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Best Local Similarity
Matches 17; Conserva
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Gaps

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probable exopolysaccharide biosynthesis protein VC0937 [imported] - Vibrio cholerae (str C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82262
C;Accession: G82262
C;Accession: J.R.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I. R.R.; Makalanns, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q9KTG5; GB:AE004176; GB:AE003852; NID:g9655385; PIDN:AAF9409º
A;Experimental source: serogroup Ol; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Length 737;
                                                                                                                                                           Length 357;
                                                                                                                                                                                               4; Indels
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     A; Reference number: S09089; MUID: 90242961; PMID: 2110531
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Pred. No. 16;
4; Mismatches
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                                                                                                                                                                                             5; Mismatches
                                                                                                                                                         Score 54;
Pred. No.
                                                                                                                                                                                                                                  7 TKKTQLQLEHLLLDLQMIL 25
                                                                                                                                                                                                                                                        40 TKKTQAELEQLLRELEQVM 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.4%;
                                                                                                                                                       Query Match 36.7%;
Best Local Similarity 52.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                          C)Genetics:
A;Introns: 12/3; 71/1; 121/3
C;Keywords: acyltransferase
                   A,Accession: S09090
A,Molecule type: protein
A,Residues: 103-122 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -737 <HEI>
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A;Molecule type: DNA
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C;Species: Mus musculus (fouse mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C;Accession: 168871
R;Matesanz, F.; Alcina, A.; Pellicer, A.
R;Matesanz, F.; Alcina, A.; Pellicer, A.
R;Matesanz, F.; Alcina, A.; Pellicer, A.
A;Reference on the control of at least five interleukin-2 molecules in different mouse strains.
A;Reference number: 154512; MUID:93307791; PMID:8319981
A;Accession: 168871
A;Accession: Isans, translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Coss-references: GB:L07576; NID:g349517; PIDN:AAA39328.1; PID:g349518
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                 A;Regidues: 1-62 <RES>
A;Crose-references: GB:L07574; NID:g349513; PIDN:AAA39326.1; PID:g349514
C;Genetics:
A;Gene: I1-2
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Pred. No. 0.18;
5; Mismatches 5; Indels
                                                                                                                                     Length 62;
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                                                                                                                                   Score 58.5; DB
Pred. No. 0.11;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.1%;
                                                                                                                                Query Match
Best Local Similarity 42.9%;
Matches 15; Conservative
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Best Local Similarity 35.6
Matches 16, Conservative
                                                                        A,Gene: 11-2
C;Superfamily: interleukin-2
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A, Molecule type:
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Gaps

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probable LygR-type regulator [imported] - Sinorhizobium meliloti (strain 1021) magaplasm C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 [C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 [C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 [R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows. Ralman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. US.A. 98, 9888, 2001 A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432 A;Accession: F95285 A;Accession: F95285 A;Accession: P95285 A;Acce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: UNIPROT: 0930K5; GB: AE006469; PIDN: AAK64848.1; PID: g14523262; GSPDB:GA; Experimental source: strain 1021, megaplasmid pSymA R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, Canin, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
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methyl-accepting chemotaxis protein VC1298 [imported] - Vibrio cholerae (strain N16961; Cispecies: Vibrio cholerae
Cispecies: Vibrio Cispecies
Cispecies: Vibrio Cholerae
Cispecies: Vi
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CiSpecies: Caenorhabditis elegans
CiSpecies: Caenorhabditis elegans
CiSpecies: On May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
CiAccession: A89130
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;ritle: Genome sequence of the neatede C. elegans: a platform for investigating biology A;Reference number: A75000; MUID:99659613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_elfA;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
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A;Molecule type: DNA
A;Residues: 1-1130 <STO>
A;Cross-references: GB:chr_V; PIDN:AAB37038.1; PID:g1086805; GSPDB:GN00023; CESP:F52E1.4
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C;Species: Caemorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22210
R;Sims, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
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Pred. No. 32;
7; Mismatches
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46.2%; Pred. No. 72;
:ive 6; Mismatches
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A;Reference number: Z19530
A;Accession: T22210
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ilarity 37.5%;
Conservative
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Matches 12; Conservative
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A;Gene: VC1298
A;Map position: 1
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-011-1998 #sequence_revision 17-011-1998 #text_change 09-011-2004
C;Accession: C70701
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Pevlin, K.; Feltwell, T.; Gentles, S.; Hamin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70701
A;Accession: C70701
A;Accession: C70701
A;Residues: 1-365 cCOL>
A;Cross-references: UNIPROT:P71599; GB:Z80233; GB:AL123456; NID:g3261645; PIDN:CAB02414.
A;Experimental source: strain H37Rv
C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. Accession: B70122

R.Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997

A.Authors: Smith, H.O.; Venter, J.C.

A.Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A.Reference number: A70100; MUID: 98065943; PMID: 9403685

A.Accession: E70122

A.Accession: E70122

A.Accession: preliminary; nucleic acid sequence not shown; translation not shown
A.Accession: L627 «KLE»

A.Residues: 1-627 «KLE»

A.Residues: 1-627 «KLE»

A.Cross-references: UNIPROT: P70859; GB: AE001129; GB: AE007183; NID: 92688071; PIDN: AAC6657
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C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                      Gaps
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7
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                                                                                                                                                                              Length 304;
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; Pred. No. 8.4;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                             STKKTOLOLE--HLLLDLOMILNGINN 30
                                                                                                                                                                                                                                                                                                                                                                   ||||| || || :| : : |||:|
STKKPQLTLEGRTVLAEARSVSNGIDN 84
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                                                                                                                                                                      34.7%;
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Best Local Similarity 42.3%;
Matches 11; Conservative
                                                                                                                                                                          Query Match
Best Local Similarity 48.18
Matches 13; Conservative
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Best Local Similarity
Matches 12; Conserv
A; Contents: annotation
                              C,Genetics:
A,Gene: SMa0353
A,Genome: plasmid
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C; Accession: AB1367
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Pictersion: AB1077; MUID:21537279; PMID:11679669
A; Accession: AB1367
A; Scatus: preliminary
A; Molecule type: DNA
A; Residues: 1-441 cGLAA
A; Residues: 1-441 cGLAA
A; Cross-references: UNIPROT:069192; GB:NC_003210; PIDN:CAD00416.1; PID:gl6411826; GSPDB:
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
Joninguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, B.; Maitournam, A.; Maiok, C.; Schlueter, T.; Sinces, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DWA
A;Residues: 1-441 -GLA>
A;Cross-references: UNIPROT:0928V0; GB:AL592022; PIDN:CAC97659.1; PID:gl6414954; GSPDB:G
A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                            C,Species: Listeria monocytogenes
C,Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aminopeptidase C [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 36;
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                                     Indels
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C,Superfamily: aminopeptidase C (bleomycin hydrolase)
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C;Superfamily: aminopeptidase C (bleomycin hydrolase)
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        32.1%; Pred. No. 14; tive 10; Mismatches
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                                                                                        3 TSSSTKKTQLQLEHLLLDLQMILNGINN
                                                                                                                           22 SSSSVLETEIVLDEIITKLNNLISEINN
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                                  Conservative
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nes 9; Conservative
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Les 9; Conserval
     Best Local Similarity
Matches 9; Conserv
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Matches
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C;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: H64307
R;Bult, C.J.; White, O; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
R;Bult, C.J.; White, O; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Rccession: H64307
A;Accession: H64307
A;Accession: H64307
A;Accession: H64307
A;Accession: H64307
A;Redus: preliminary; nucleic acid sequence not shown; translation not shown
A;Redus: 1-189 <BUL>
A;Cross-references: UNIPROT:Q60376; GB:U67464; GB:L77117; NID:g1590852; PIDN:AAB98051.1;
C;Genetics:
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A; Residues: 1-240 <WILD>
A; Cross-references: UNIPROT:Q20417; EMBL:Z49910; PIDN:CAA90123.1; GSPDB:GN0020; CESP:F4
A; Experimental source: clone F44G4
C; Genetics: CESP: F44G4.7
A; Gene: CESP: F44G4.7
A; Map position: 2
A; Introns: 123/2; 159/3
C; Superfamily: Caenorhabditis elegans hypothetical protein F44G4.7
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: F64145
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                                                                                                                                                                                                                                                                                                               Length 240;
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preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                   2 PTSSSTKKTQLQLEHLLLDLQMILN 26
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Best Local Similarity 44.0%;
Matches 11; Conservative
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C;Date: Cnlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86548
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; It
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: F86548
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-938 <STO>
A;Coses-reference
                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q9Z883; GB:BA000008; NID:g8978836; PIDN:BAA98772.1; GSPDB:GRA;Edencial source: strain J138
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymorphic membrane protein E/F family CP0286 [imported] - Chlamydophila pneumoniae (st C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (5.5pecies: Chlamydophila pneumoniae, Chlamydia pneumoniae (5.5pecies: Chlamydophila pneumoniae, C;Species: Chlamydophila pneumoniae, C;Species: Chlamydophila pneumoniae, C;Accession: H72074; E81593 R;Kalman, S; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J., Astrie Comparative genomes of Clamydia pneumoniae and C. trachomatis.
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A; Residues: 1-938 <ARN>
A; Residues: 1-938 <ARN>
A; Cross-references: UNID: 922883; GB: AE001631; GB: AE001363; NID: 94376750; PIDN: AAD1860
A; Experimental source: strain CWL029
B; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Agids Res. 28, 1397-1406, 2000
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A;Residues: 1-938 «REA>
A;Cross-references: GB:AE002190; GB:AE002161; NID:g7189209; PIDN:AAF38143.1; PID:g718921
A;Experimental source: strain AR39, HL cells
C;Genetics:
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C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: H82447
R;Heidelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J., Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A,Reference number: A81500; MUID:20150255; PMID:10684935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47.5; DE Pred. No. 98; 4; Mismatches
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42.9%;
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Best Local Similarity
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Best Local Similarity
Local 12; Conserv
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                                                                                                                                                                                                        C;Species: simian immunodeficiency virus, STV
C;Date: 30-Jun-1889 #sequence_revision 30-Jun-1889 #text_change 03-Jun-2002
C;Date: 30-Jun-1889 #sequence_revision 30-Jun-1889 #text_change 03-Jun-2002
C;Date: 30-Jun-1889 #sequence_revision 30-Jun-1889 #text_change 03-Jun-2002
R;Paceasawa, M.; Miura, T.; Hasegawa, A.; Morikawa, S.; Tsujimoto, H.; Miki, K.; Kitamura
Nature 333, 457-461, 1988
A;Fitle: Sequence of simian immunodeficiency virus from African green monkey, a new memb
A;Reference number: A30045; MUD:88232906; PMID:3374586
A;Accession: B30045
A;Residues: 1-1061 <FUX>
A;Residues: 1-1061 <FUX>
C;Cosesion: Specific enzymatic cleavages may yield mature proteins including protease, re
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F86548
polymorphic outer membrane protein E family [imported] - Chlamydophila pneumoniae (strai
                                                                                                                                              IV-1 retropepsin (EC 3.4.23.16) - simian immunodeficiency virus (African green monkey i Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA poly; Species: simian immunodeficiency virus, SIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Superfamily: pol polyprotein
C;Keywords: aspartic proteinase; hydrolase; nucleotidyltransferase; polyprotein; reverse
P;111-210/Product: retropepsin #status predicted <RTP>
P;134/Active site: Asp (shared with dimeric partner) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein SPBC21D10.13 SPBC1921.07c – fission yeast (Schizosaccharomyces pomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AL122033; PIDN:CAB58973.1; GSPDB:GN00067; SPDB:SPBC1921.07c C;Genetics:
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Date: 16-Jul-1999 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
Accession: T11685; T39791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status; preliminary; translated from GB/EMBL/DDBJ
A;Ratus; preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1.155 cSEE>
A;Cross-references: UNIPROT:Q9USW9; EMBL:AL031536; NID:e1319499
A;Experimental source: strain 972h(-)
R;Seeger, K; Harris, D: McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Bubmitted to the EMBL Data Library, October 1999
A;Reference number: Z21816
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Pred. No. 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
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Best Local Similarity 52.9%;
Matches 9; Conservative
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Best Local Similarity 45.8%;
Matches 11; Conservative
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A;Accession: T11685
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 129-244 <SE2>
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                                                   Score 47;
Pred. No.
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440 QLDLEHLALERQIDLDG 456
                                                                                                                                                                                       11 QLQLEHLLLDLQMILNG 27
                                                   32.0%;
58.8%;
                                               Query Match
Best Local Similarity 58.8 Matches 10; Conservative
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nes 12; Conserv
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Cipecies: Staphylococcus aureus
Cipate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
Cipate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
Cipate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
Cipate: 10-May-2001
Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Tuoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Residues: DA
A;Residues: 1-557 <KUR>
A;Residues: 1-557 <KUR>
A;Residues: 1-557 <KUR>
C;Genetics:
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R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White Snow, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt., Bon, D.); Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt., Sowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Mature 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Anticle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; MUID: 98055943; PMID: 9403685
A; Accession: B70209
A; Assiduary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Mosicule type: DNA
A; Residuars: 1-398 «KLES
A; Gross-references: UNIPROT: O50911; GB: AE000790; NID: 92690224; PIDN: AAC66245.1; PID: 9268
A; Experimental source: strain B31
C; Genetics:
A; G
                                            A;Accession: HB2447
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-230 <HBIS
A;Croser-references: UNIPROT:O9KM56; GB:AE004384; GB:AE003853; NID:g9657936; PIDN:AAF9643
A;Experimental source: serogroup Ol; strain N16961; biotype El Tor
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C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004 C;Accession: B70209
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 2; Length 230;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                           A;Map position: 2
C;Superfamily: ompR protein; response regulator homology
Reference number: A82035; MUID:20406833; PMID:10952301
Accession: H82447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
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||22 APSTESVEQTRFELGDLVLDL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APTSSSTKKTQLQLEHLLLDL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 42.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                  C,Genetics:
A,Gene: VCA0532
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A;Gene: SA0640
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A;Accession: T41244
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosicuse: 1-1008 <LYN>
A;Mosicuse: 1-1008 <LYN>
A;Cross-references: UNIPROT:Q9UU99; EMBL:AL109608; PIDN:CAB51563.1; GSPDB:GN00068; SPDB:A;Experimental source: strain 972h-; cosmid c23B6
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A;Residues: 1-1964 <BHA>
A;Cross-references: UNIEROT:093522; GB:AF055895; NID:g3660671; PIDN:AAC83556.1; PID:g366.
A;Cross-references: UNIEROT:093522; GB:AF055895; NID:g3660671; PIDN:AAC83556.1; PID:g366.
A;Cross-referental source: cell line XTC
C;Superfemnity: myosin heavy chain; myosin motor domain homology
P;84-764/Domain: myosin motor domain homology <MMO>
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R;Bhati.Dey, N.; Taira, M.; Conti, M.A.; Nooruddin, H.; Adelstein, R.S.
R;Bhati.Dey, 78, 33-36, 1998
A;Itle: Differential expression of non-muscle myosin heavy chain genes during Xenopus A;Reference number: A59282; MUID:99077683; PMID:9858676
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                                                                                                                                                                                                                                                            - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                      RESULT 37
T05656
hypothetical protein F22I13.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nonmuscle myosin II heavy chain A - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
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F;639-822/Domain: cellular retinaldehyde-binding protein homology
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A; Status: preliminary; not compared with conceptual translation A; Molecule type: mRNA
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4; Indels
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A,Gene: jhp0321
C,Superfamily: conserved hypothetical protein HI0176
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Job time : 24.6066 BecB
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C'Species: O'Species: O'S C'SPECIES (STEED CONTROL C
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A,Variety: strain J99
A,Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: A71946
A;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MuID:99120557; PMID:9923682
A;Accession: A71946
A;Accession: A71846
A;Accession: A71946
A;
R;Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F
submitted to the Protein Sequence Database, February 1999
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A;Mosidues: 1-159 <BEV>
A;Crost-references: UNIPROT:Q9SVF7; EMBL:AL035539
A;Crostimental source: cultivar Columbia; BAC clone F22I13
C;Genetics:
A;Map position: 4
A;Introns: 117/1
A;Note: F22I13.50
C;Superfamily: Arabidopsis thaliana hypothetical protein F22I13.50
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C,Species: Helicobacter pylori
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                                                                                            A;Reference number: Z15420
A;Accession: T05656
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-323 <KUR>
A;Cross-references: UNIPROT:Q97VK9; GB:AE006641; NID:g13815920; PIDN:AAK42735.1; GSPDB:c
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                                                                                                                                                                                                                                                                                                                                                          C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H90434
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Score 46; DB 2; Length 293;
Pred. No. 44;
3; Mismatches 6; Indels
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148 KKTYLALAHGLVDKSIIIN 166
                                                                                                                       8 KKTQLQLEHLLLDLQMILN 26
   Query Match 31.3%;
Best Local Similarity 52.6%;
Matches 10; Conservative
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sus scrofa
meriones un
lama glama
equus cabal
homo sapien
orcinus orc
homo eapien
delphinapte
cavia porce
ovis aries
bos taurus
bubalus bub
capra hircu
bos taurus
ovis aries
bos taurus
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canis famil
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haemophilus
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Q96fuy5

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PCAP HUMAN
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Q8R6R8
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1112 RAT
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1112 HORSE
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Q0E6220
Q0E6220
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ILI2_BOVIN
ILI2_SHEBP
Q0E1XR7
Q0GHYR7
ILI2_CEREL
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Copyright (c) 1993 - 2005 Compugen Ltd.
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112_MIRAN
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FROM N.A.

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MEDLINE=84247353; PubMed=6330695;
Holbrook N.J., Lieber M., Crabtree G.R.;
Holbrook N.J., If the filanking region of the human interleukin 2 gene: homologies with adult T-cell leukemia virus.";
Nucleic Acids Res. 12:5005-5013(1984).
                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=20545237; PubMed=11093171;
DOI=10.1002/1521-4141(2000012)30:12<3516::AID-IMMU3516>3.0.CO;2-S;
                                                                                 Incerteuring Control Homen).

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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P60568; P01585;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Manbiline=81167472; PubMed=6403867;
Taniguchi T., Matsui H., Fujita T., Takaoka C., Kashima N.,
Yoshimoto R., Hamuro J.;
                                                                                                                                                                                                                                                                                                                                                                Length 150;
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                                                                                                                                                                                                                         GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
                                                                     Last annotation update)
                                                          sequence update)
                                                                                                                                                                                                                                                                                                                                                              96.7%; Score 147; DB 2; I
100.0%; Pred. No. 8.5e-14;
ive 0; Mismatches 0;
                                                                                                                                                                        Matesanz F., Delgado C., Fresno M., Alcina A.; "Allelic selection of human IL-2 gene."; "Lur. J. Immunol. 30.3516-3521(2000).
EMBL; AF228636; AAGS3575.1; -.
                             150 AA.
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InterPro, IPR000779; Interleukin-2.
Pfam; PP00715; IL2; 1.
                                                Created)
                            PRT;
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ProDom; PD003649; Interleukin-2; 1.
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PROSITE; PS00424; INTERLEUKIN_2; 1.
                                                           Last
                                             01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
Interleukin-2 (Fragment).
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Best Local Similarity 100.
Matches 30, Conservative
                           PRELIMINARY;
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A KEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Bhat N.K.,
A Boxidench D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Halton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachay J., Helton B.K., Retreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human
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MEDI-INE=6422299; PubMed=8824916;
MEDI-INE=6422299; PubMed=8824916;
DOI=1.01002/(SII) 1098-2795(199602)43:2<180::AID-MRD7>3.3.CO;2-D;
Chernicky C.L., Tan H., Burfeind P., Ilan J., Ilan J.;
"Sequence of interleukin-2 isolated from human placental poly A+ RNA:
possible role in maintenance of fetal allograft.";
Mol. Reprod. Dev. 43:180(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holbrook N.J., Smith K.A., Fornace A.J. Jr., Comeau C.M., Wiskocil R.L., Crabtree G.R., Fornace A.J. Jr., Comeau C.M., "T-cell growth factor: complete nucleotide sequence and organization of the gene in normal and malignant cells.", Proc. Natl. Acad. Sci. U.S.A. 81:1634-1638(1984).
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Fujimoto K., Teranishi T., Hirano T., Onoue K.;
"Cloning of interleukin 2 mRNAs from human tonsils.";
Biochem. Biophys. Res. Commun. 115:1040-1047(1983).
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"Interleukin-2 transcripts in human and rodent brains: possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=84170243; PubMed=6324170;
Flita T., Takaoka C., Matsui H., Taniguchi T.;
"Structure of the human interleukin 2 gene.";
Proc. Natl. Acad. Sci. U.S.A. 80:7437-7441(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 11:4307-4323(1983)
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MEDLINE=84170356; PubMed=6608729;
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MEDLINE=95239150; PubMed=7722480;
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J. Neurochem. 64:1928-1936(1995)
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                                                                                                                                                    SECUENCE OF 1-69 FROM N.A.

MEDLINE=87064618; PubMed=3491296;
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Kamoun M., Kant J.A., Crabtree G.R.;
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changes and confers inducibility on chloramphenicol acetyltransferase
gene during activation of T cells ";
Mol. Cell. Biol. 6:3042-3049(1986).
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MEDLINE=95111955; PubMed=7529123;
MEDLINE=95111955; PubMed=7529123;
Branborough P., Hedgecock C.J., Richards W.G.;
Branborough P., Hedgecock C.J., Richards W.G.;
Branborough P., Hedgecock C.J., Richards W.G.;
modelling ";
Structure 2:8199-851(1994).
-i- FUNCTION: Produced by T-cells in response to antigenic or
mitogenic stimulation, this protein is required for T-cell
                                                          MEDLINE=89062420; PubMed=3264184;
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"Structure-activity relationships of recombinant human interleukin
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 21-153, DISULFIDE BOND, AND CARBOHYDRATE-LINKAGE SITE. MEDIINE=85038540; PubMed=6333684; PubMed=6333684; Medium R.W., Runy R.M., Panico M., Morris H.R., Chowdhry V.; "Amino acid sequence and post-translational modification of human interleukin 2.";
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Nishino N., Obaru K., Maeda S., Shimada K., Onoue K.;
"Organization of the DNA regions flanking the human interleukin 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYDRATE-LINKAGE SITE.
MEDLINE-90008901; PubMed-2793860;
Conradt H.S., Nimtz M., Dittmar K.E.J., Lindenmaier W., Hoppe J.,
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MEDILINE=22379010; Pubmed=1510960;
MOCH H.R., Driscoll P.C., Boyd J., Cooke R.M., Weir M.P.,
Campbell I.D.;
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MEDLINE=92335891; PubMed=1631562;
                                                                                                                          Biochemistry 27:6883-6892(1988).
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Biochemistry 31:7741-7744(1992).
                                                                                                                                                                                                                                                                                                                                                               Biomed. Res. 6:197-205(1985).
                                               SEQUENCE OF 21-153 FROM N.A.
 mouse cDNA sequences.";
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        unmune response. Can stitulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.
SUBCELLULAR LOCATION: Secreted.
SUBCELLULAR LOCATION: Secreted.
SUBCELLULAR LOCATION: Secreted.
(T-ALL) by a chromosomal translocation t(4;16)(q26;p13) which pinvolves TNFSF17 and IL2.
Involves TNFSF17 and IL2.
SIMILARITY: Belongs to the IL2 family.
SIMILARITY: Belongs to the IL2 family.
SIMILARITY: Belongs to the IL2 family.
MWM="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=206".
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proliferation and other activities crucial to regulation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
NCBI_TaxID=9580;
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InterPro; IPR000779; Interleukin-2.
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MEDINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MALSCHUL S.F., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jedena H., Moore T., Max S.I., Wang J., Haleh F.,

A Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

Bromstein M.J., Ubdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzley D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Miland M.J., Marra M.A.,

Maria M.J., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human mouse conva sequences."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                  PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
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59E2F40F25860F84 CRC64;
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:000515; F:immune response; IEA.
InterPro; IPR009079; 4_helix_cytokine.
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Last annotation update)
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100.0%; Pred. No. 8.7e-14;
iive 0; Mismatches 0;
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O-linked (GalNAc.
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                                                           InterPro; IPR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
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153 In
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17628 MW;
                     EMBL; M11144; AAA35454.1; -.
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TISSUE=PCR rescued clones;
Strausberg R.;
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Best Local Similarity 100.0
Matches 30, Conservative
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23
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153 AA;
                                         PIR; A94067; ICGI2
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SEQUENCE
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Interleukin-2.
O-linked (GalNac. . .) (By similarity).
9 similarity.
; 7853FE624A5E4A49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
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05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.7%; Score 147; DB 1; Length 154; 100.0%; Pred. No. 8.8e-14; ive 0; Mismatches 0; Indels
                                                                                                                                                                       Length 153;
                                                                                                                                                                                                                      Indels
                                                                                                                      1942F50F25960E88 CRC64;
                                                                                                                                                                  96.7%; Score 147; DB 2; I
100.0%; Pred. No. 8.7e-14;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  154 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                2 APTSSSTKKTQLQLEHLLLDLQMILNGINN 31
                                                                                                                                                                                                                                                                                           21 APTSSSTKKTQLQLEHLLLDLQMILNGINN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR000779; Interleukin-2.
Pfam; PP00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
SWART; SM00189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 153 AA; 17597 MW; 1942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 35, Created)
(Rel. 35, Last seq
(Rel. 44, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 AA; 17686 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D63352; BAA09676.1; -. HSSP; P01585; 1M49.
                                                                                                                                                                                                                 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
154
23
126
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                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997
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KESULT 6 IL2\_MACMU

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                                                                                                                                                                                                                                                                                                                                                                  nonhuman primates.", 3954(1995).

1. Immunol. 155:1946-3954(1995).

1. FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to requiation of the immune response. Can stimulate B cells, monocytes, lymphokineactivated killer cells, natural killer cells, and glioma cells (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          By similarity.
Interleukin-2.
O-linked (GalNAc. . .) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U00511;
U00511;
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2004 (Rel. 44, Last annotation update)
05-UUL-2004 (Rel. 44, Last annotation update)
1nterleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
Name=IL2; Synonyms=IL-2;
Papio anubis (Olive baboon).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                  macaca nemestrina (Pig-talled macaque).
Bukaryota, Metazoa, Chordata; Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates; Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                            Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TGGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          By similarity.
GAEBA480F204BA49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 147; DB 1; I
Pred. No. 8.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULÂR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 APTSSSTKKTOLOLEHLLLDLOMILNGINN
                                                                                                                         Macaca nemestrina (Pig-tailed macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR000779; Interleukin-2.
                                                                                                                                                                                                                                                                                                     MEDLINE=96003435; PubMed=7561102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 AA; 17685 MW;
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HSSP; P01585; 1M48.
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                                                                                                                                                                                         Cercopithecinae; Macaca.
NCBI_TaxID=9545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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154
23
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
P68290; P51498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity)
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Q865Y1;
                                                                                                          Name=IL2;
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110 1112 PA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inmunol. 155:3946-3954(1995).
FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine activated killer cells, natural killer cells, and glioma cells (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin-2.
O-linked (GalNAc. . .) (By similarity)
                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and nonhuman primates.";
J. Immunol. 155:3946-3954(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                P68201; P51498;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          By similarity.
6AEBA480F204BA49 CRC64;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sumidatity).
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                    154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. ...
                                               21 APTSSSTKKTQLQLEHLLLDLQMILNGINN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 APTSSSTKKTQLQLEHLLLDLQMILNGINN 31
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                  APTSSSTKKTQLQLEHLLLDLQMILNGINN
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InterPro; IPR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96003435; PubMed=7561102;
                                                                                                                                                                                                                                                                                                                       Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00265; INTERLEUKIN2.
SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17685 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30; Conservative
                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecinae; Macaca.
NCBI_TaxID=9544;
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154
23
126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 AA;
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ID_ IL2_MACNE
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Gaps

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154 AA

PRT;

STANDARD;

CARBOHYD DISULFID SEQUENCE Query Match

Matches

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-cell. SIGNAL

Length 154; IndelB

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                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells (By
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 20 By similarity.
21 154 Interleukin-2.
78 126 By similarity.
23 23 0-linked (GalNAc. . .) (By similarity).
154 AA; 17657 MW; AA642BABBCA87569 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
Patarroyo M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Platyrrhini, Cebidae, Aotinae, Aotus.
                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 145; DB 1; Length 154;
Pred. No. 1.8e-13;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, U88364; AAD41534.1; -...
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR009079; Interleukin-2.
Pfam; PF00715; IL2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actus lemurinus (Northern gray-necked night monkey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 AA
                                                                     SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.86
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
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                                                                                                                                                                                                                                                                             InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR000779; Interleukin-2.
Pfam; PR00715; IL2; I.
PRINTS; PR00265; INTERLEUKIN2.
PRODOM; PD003649; Interleukin-2; I.
SMART; SM00189; IL2; I.
                                           SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                              EMBL; AF294755; AAK92042.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.4%;
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es 29; Conserv
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                                    similarity)
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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SIGNAL
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                -1- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine activated killer cells, natural killer cells, and glioma cells (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Platyrxhini, Cebidae, Cebinae, Saimiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heraud J.M., Lavergne A., Kazanji M.;
"Molecular cloning, characterization, and quantification of squirrel monkey (Saminis sciureus) Thl and Th2 cytokines.";
Immunogenetics 54:20-29(2002).
-!- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
O-linked (GalNAc. . .) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=21972723; PubMed=11976788; DOI=10.1007/800251-002-0443-y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 response; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 147; DB 1; Length 154;
Pred. No. 8.8e-14;
                                                                 Villinger F.; "Nonhuman primate cytokines."; "Nonhuman primate cytokines."; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47F486BDF204AD6E CRC64;
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Cytokine; Glycoprotein; Growth factor; Immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.7%; Scot.
100.0%; Pred. No. c
0; Mismatches
                                                                                                                                                                                                                           -!- SUBCELLULĀR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.
Interleukin-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 APTSSSTKKTQLQLEHLLLDLQMILNGINN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 APTSSSTKKTQLQLEHLLLDLQMILNGINN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saimiri sciureus (Common squirrel monkey)
                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; POISBS; 1M49.
InterPro; IRRO09079; 4 helix cytokine.
InterPro; IPR009779; Interleukin-2.
Pfam; PF00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
PRODOM; PD003649; Interleukin-2; 1.
SWART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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154
126
 Cercopithecinae; Papio.
                                                  SEQUENCE FROM N.A.
              NCBI_TaxID=9555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9521;
                                                                                                                                                                                                             similarity)
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21
78
23
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Q8MKH2;
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IL2 SAISC
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Score 145; DB 2; Length 154;
Pred. No. 1.8e-13;
1; Mismatches 0; Indels
   Query Match
Best Local Similarity 96.7
Matches 29; Conservative
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Gaps

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Q7JFM3

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[1]
SEQUENCE FROM N.A.
Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
Patarroyo M.E.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U88361; ARD41535.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A., Patazroyo M.E.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U88365; AAD41538.1; -.
HSSP; P60568; IIRL.
GO; GO:0005576; Cextracellular; IRA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0005955; P:immune response; IRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Aotus nancymaae (Ma's night monkey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Platyrrhini, Cebidae, Aotinae, Aotus.
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Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
                                          Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.4%; Score 145; DB 2; Length 154; 96.7%; Pred. No. 1.8e-13; live 1; Mismatches 0; Indels
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GO; GO:00055134; F:interleukin-2 receptor binding; IEA.

GO; GO:00055134; F:interleukin-2 receptor binding; IEA.

GO; GO:0006955; P:immune response; IEA.

GO; GO:00069079; Interleukin-2.

InterPro; IPR000779; Interleukin-2.

PEMN; PR00755; INTERLEUKIN2.

ProDom; PD003649; Interleukin-2; 1.

PRINTS; PR00365; INTERLEUKIN2.

PROSITE; PS00424; INTERLEUKIN 2; 1.

PROSITE; PS00424; INTERLEUKIN 2; 1.

SEQUENCE 154 AA; 17675 MW; AB552ABBADA96469 CRC64;
                                                                                       0; Indels
154 AA; 17675 MW; AB752ABBADA96469 CRC64;
                                                                                                                                                                                                                                                                                                                                    05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                          Score 145; DB 2;
Pred. No. 1.8e-13;
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                                        Query Match 95.4%; Score 145; DB Best Local Similarity 96.7%; Pred. No. 1.8e Matches 29; Conservative 1; Mismatches
                                                                                                                                                              21 APTSSSTKKTQLQLEHLLLDLQMLLNGINN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 APTSSSTKKTQLQLEHLLLDLQMLLNGINN 50
                                                                                                                                    2 APTSSSTKKTQLQLEHLLLDLQMILNGINN 31
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01-NOV-1999 (TrEMBLrel. 12, Last seq
                                                                                                                                                                                                                                                                                                PRT;
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Best Local Similarity 96.7%
                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=37293;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                        Q7JFM5;
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Amillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
Amillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
Batairoyo M.E.,
Submitted (FBB-1997) to the EWEL/GenBank/DDBJ databases.
BRG; GO:0005556; C:extracellular, IEA.
BRG; GO:0005134; F:interleukin-2 receptor binding; IEA.
RG; GO:0006955; P:immune response; IEA.
BRG; GO:0006955; P:immune response; IEA.
BRITERPEO; IFM000779; Interleukin-2.
BRINTS; PR000565; IWTERLEUKIN2.
BRODA; PRODA; J. 1.2; 1.
BRODA; PRODA; J. 1.2; 1.
BRODA; PRODA; J. 1.2; 1.
BROSITE; PS00424; INTERLEUKIN 2; 1.
SWART; SWO0189; ILZ; 1.
SRAKET; SWO0189; ILZ; 1.
SRAKET; SWO0189; ILZ; 1.
SRAKET; SWO0189; ILZ; 1.
SRAKET; SWOUNEVER INTERLEUKIN 2; 1.
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Mutillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A., Patarroyo M.E.; Hernandez E., Echeverry S.J., Mendez J.A., Moreno A., Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

EMBL, 108362; AAD41537.1; -.

GO, GO:000515; C:extracellular; IEA.

GO, GO:000515; F:interleukin-2 receptor binding; IEA.

GO, GO:000615; P:immune response; IEA.

InterPro; IPR00979; 4 helix cytokine.

InterPro; IPR009779; Interleukin-2.

Pfam; PF00715; IL2; 1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
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                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Match 95.4%; Score 145; DB 2; L. Local Similarity 96.7%; Pred. No. 1.8e-13; es 29; Conservative 1; Mismatches 0;
                                                                                                                                                                            154 AA
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                                        21 APTSSSTKKTQLQLEHLLLDLQMLINGINN 50
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                2 APTSSSTKKTQLQLEHLLLDLQMILNGINN 31
                                                                                                                                                                                                                                                                                                              Actus nigriceps (Black-headed owl monkey).
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                                                                                                                                                                            PRT;
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ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; ILZ; 1.
PROSITE; PS00424; INTERLEUKIN_2; 1.
                                                                                                                                                                            PRELIMINARY;
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CARBOHYD
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interleukin-2.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chikara S.K., Sharma G.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AYS23040; AAS17753.1;
GO, GO:0005756; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0005955; P:immen response; IEA.
InterPro; IRR009079; 4 helix cytckine.
InterPro; IPR000779; Interleukin-2.
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY283686; AAP35033.1; -
                                        Pfam; PF00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003189; IL2; 1.
SMART; SMO0189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 133 AA; 15462 MW; 1699F680A09DB3B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     133 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PTSSSTKKTQLQLEHLLLDLQMILNGINN 30
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                                                                                                                                                                                                                                                                                              21 APTSSSTKKTQLQLEHLLLDLQMLLNGINN
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR000779; Interleukin-2.
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PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interleukin-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Q6QWN0
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Q7Z7M3
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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-!- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activited killer cells, matural killer cells, and glioma cells.
-!- SUBCELDULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-2 family.
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Interleukin-2.
O-linked (GalNAc. . .) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A. "Comparative sequence analysis of cytokine genes from human and
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TGGF).
                                                                                                                                                                                                                                                                                                                                                     Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                         SMART; SM00189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 133 AA; 15461 MW; 1699FRA880959B90 CRC64;
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                               94.1%; Score 143; DB 2;
100.0%; Pred. No. 3e-13;
live 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 PTSSSTKKTQLQLEHLLLDLQMILNGINN 31
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InterPro; IPR000779; Interleukin-2.
Pfam; PR00715; IL2; IL.
PRINTS; PR00265; INTERLEUKIN2.
PRODOM; PD003649; Interleukin-2; I.
SWART; SM00189; IL2; I.
                                                                                                 cytokine.
                                                                                                                                                            Pfam; PF00715; IL2; 1.
ProDom; PD003649; Interleukin-2; 1.
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                                                                                              InterPro, IPR009079; 4 helix cytoki
InterPro, IPR000779; Interleukin-2.
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                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.(
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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154
23
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METAURDETOR R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

MIschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

MIschall S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

MISCHORD, M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

MISCHORD, M., Soares M.B., Peters G.J., Abramson R.D., Mullahy S.J.,

MISCHARD, M. Morley M.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

MILLIAND D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Milalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Milalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Milalon M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milalon M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

MILLING M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

MILLING M., Marra M.J., Schmutz J., Myers R.M., Butterfield Y.S.,

MILLING M.J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

M. A., Marra M.J., Schmutz J., Myers R.M., Schein J.E.,

Jones S.J., Marra M.J.,

M. A., Marra M.J.,

M. M., Marra M.J.,
                                                                                                                                           ö
                                                                                                                                           Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                           ö
                                                                                             93.4%; Score 142; DB 1; Length 154; 96.7%; Pred. No. 4.9e-13; live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.1%; Score 137; DB 2; Length 153; Best Local Similarity 96.7%; Pred. No. 2.7e-12; Matches 29; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

TISSUE-PCR rescued clones;
Strauberg R.;
Strauberg R.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC066556; ARH66556.1; -.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR009079; 4 helix cytokine.
78 126 By similarity.
25 25 R >> 8.74
74 74 K >> E.
154 AA, 17754 MW, 9FBB51814204BA48 CRC64;
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Prodom; PD003449; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 153 AA; 17644 MW; 59F9980409964F84 CRC64;
                                                                                                                                                                                                                                                                                                                                                           05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                         153 AA
                                                                                                                                                                                                     APTSRSTKKTQLQLEHLLLDLQMILNGINN 50
                                                                                                                                                                                2 APTSSSTKKTQLQLEHLLLDLQMILNGINN 31
                                                                          Query Match
Best Local Similarity 96.7,
Best Local 29; Conservative
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                         Interleukin 2,.
                    VARIANT
VARIANT
SEQUENCE
  DISULFID
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SEQUENCE FROM N.A.

Xu D., Wu Y., Chen J., Yu L., Zhong M., Hui Y., Qu H.;
"Expression of human IL-2 from gene transferred mouse melanoma cells and its effect on the growth of mouse melanoma.";
Chin. J. Microbiol. Immunol. 13:78-82(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R GO; GO:0005576; C:extracellular; TAS.
R GO; GO:0015134; F:interleukin-2 receptor binding; TAS.
R GO; GO:0015134; F:interleukin-2 receptor binding; TAS.
R GO; GO:0015109; F:intiase activator activity; TAS.
R GO; GO:0006916; P:anti-apoptosis; TAS.
R GO; GO:0007267; P:cell.cell signaling; TAS.
R GO; GO:001010; P:immune response; TAS.
R GO; GO:001010; P:immune response; TAS.
R GO; GO:0010307; P:positive regulation of cell growth; TAS.
R GO; GO:0010317; P:positive regulation of cell proliferation; TAS.
R GO; GO:0010317; P:T-cell differentiation; TAS.
R InterPro; IPR000779; Interleukin-2.
R InterPro; IPR000779; Interleukin-2.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu L.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
EMBL; U25676; AAA70092.1; -.
HSSP; P60568; 1IRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SW00189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 156 AA; 18002 MW; 8E0452D43B336389 CRC64;
                                                                                                                                                                                    (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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21 ALTSSTKKTQLQLEHLLLDLQMILNGINN 50
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                                                                                                                                         PRT;
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Name=IL-2;
                                                                                                                                                                                                                                                                                          Name=1L2;
Homo sapiens (Human).
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SEQUENCE FROM N.A.
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Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                         01-NOV-1996
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01-MAR-2004
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"Sequence and characterization of phocine interleukin 2.";
"In Wildl. Dis. 34:81-90(1998)
"In Middl. Dis. 34:81-90(1998)
"In Middl. Dis. 34:81-90(1998)
"In Middl. Dis. 34:81-90(1998)
"In Middl. Dis. 34:81-90(1998)
"In Middle Stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokineativated killer cells, natural killer cells, and glioma cells (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Pinnipedia, Phocidae, Mirounga.
MEDLINE=95239150; PubMed=7722480;
Eizenberg O., Faber-Elman A., Lotan M., Schwartz M.;
"Interleukin-2 transcripts in human and rodent brains: possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               139 AA; 15986 MW; 731FBA406D0C63C5 CRC64;
                                                                  expression by astrocytes.";
J. Neurochem. 64:1928-1936(1995).
BMBL: 577433, AAD14264.1;
GO; GO:0005576; C:extracellular; IEA.
GO; GO:000514; F:interleukhn-2 receptor binding; IEA.
GO; GO:0005955; P:imterleukhn-2 receptor linterPro; IPR009079; 4 helix cytokine.
InterPro; IPR000779; Interleukhn-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.2%; Score 134; DB 2; L6 93.3%; Pred. No. 6.9e-12; ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mirounga angustirostris (Northern elephant seal).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 APTSSSTKKTQLXLEHLLLDLQMILXGINN 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 APTSSSTKKTQLQLEHLLLDLQMILNGINN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR000779; Interleukin-2.
Pfam; PR00715; IL2; I.
PRIWTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
                                                                                                                                                                                                                                                                                                         PRINTS; PRO0265; INTERLEUKIN2.
ProDom; PRO03649; Interleukin-2; 1.
SWART; SMO0189; ILL2; 1.
PROSITE; PSO0424; INTERLEUKIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98136706; PubMed=9476229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U79187; AAC12258.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 93.3
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                   Pfam; PF00715; IL2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID=9716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 MIRAN
062641;
                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=IL2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-9335676; PubMed-8352761;
Cozzi P.J., Padrid P.A., Takeda J., Alegre M.-A., Yuhki N., Leff A.R.;
"Sequence and functional characterization of feline interleukin 2.";
"Sequence and functional 194:1038-1043(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Litman R., Gibbs C., Good R.A., Day N.K.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to requistion of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.
-! SUBCELIULAR LOCATION: Secreted.
-! SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                    . .) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Pelidae, Felis.
NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00424, INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TGGF)
                                                                                                                                                                                                                                          Score 116; DB 1; Length 154;
Pred. No. 3.9e-09;
6; Mismatches 2; Indels
                                                                                                           Interleukin-2.
O-linked (GalNAc. . .) (By
By similarity.
0C92337A4B16B6BB CRC64;
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Interleukin-2.
By similarity.
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                                                                               By similarity.
                                                                                                                                                                                                                                                                                                                                                                                     21 APTISSTKETQQQLEQLLLDLRLLLLNGVNN 50
                                                                                                                                                                                                                                                                                                                                                         2 APTSSSTKKTQLQLEHLLLDLQMILNGINN 31
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HSSP; P01585; 1M49.

InterPro; IPR000709; 4 helix cytokine.

InterPro; IPR000779; Interleukin-2.

Pfam; PF00715; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
                                                                                                                                                                                          154 AA; 17661 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Felis silvestris catus (Cat).
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                                                                                                                                                                                                                                                76.38;
                                                                                                                                                                                                                                                                         73.38;
                                                                                                                                                                                                                                                                    Best Local Similarity 73.3
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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154
23
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154
126
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78
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CHAIN
DISULPID
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                MEDLINE=99221046; PubMed=10206205; DOI=10.1016/S0165-2427(99)00009-4; St-Laurent G., Beliveau C., Archambault D.; "Molecular cloning and phylogenetic analysis of beluga whale (Delphinapterus leucas) and grey seal (Hallchoerus grypus) interleukin
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Pinnipedia, Phocidae, Halichoerus.
N-linked (GlCNAc. . ) (Potential).

KI -> RM (in Ref. 2).

F -> I (in Ref. 2).

; 2E71E3BDBB9665EF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 155;
                                                       Length 154;
                                                      Score 114; DB 1; Length 15
Pred. No. 7.7e-09;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD003649; Interleukin-2; 1.
SWART; SM0189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 155 AA; 17860 MW; F18F449AC672241A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR009079; 4 halix cytokine.
InterPro; IPR000779; Interleukin-2.
                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Interleukin 2 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.4%; Score 108.5; DB 2; Best Local Similarity 74.2%; Pred. No. 5.2e-08; Matches 23; Conservative 5; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                      Vet. Immunol. Immunopathol. 67:385-394(1999)
EMBL; AF072871; AAD40848.1; -.
HSSP; P60568; IIRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 AA.
                                                                                                                                                                               155 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 APTTSSSTKETQQQLEQLLLDLRLLLNGVNN 51
                                                                                                               21 APASSSTKETQQQLEQLLLDLRLLLNGVNN 50
                                                                                                    2 APTSSSTKKTQLQLEHLLLDLQMILNGINN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
IISSUE=Blood;
Markus S., Groene A., Baumgaertner W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                               PRT;
111 111 N-:
3 4 KI
150 150 F ·
154 AA; 17653 MW;
                                                                                                                                                                                                                                              Halichoerus grypus (Gray seal).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00265; INTERLEUKIN2
                                                      75.0%;
73.3%;
                                         Query Match
Best Local Similarity 73.3%,
Conservative
                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00715; IL2;
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 NCBI_TaxID=9711;
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                                                                                                                                                                                                                                     Interleukin 2.
          CONFLICT
                                SEQUENCE
 CARBOHYD
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Q9BG74;
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Q9BG74
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A single nucleotide insertion in the canine interleukin-2 receptor gamma chain results in X-linked severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112_CANFA STANDARD; PRT; 155 AA. (22946; 028249; 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-2004 (Rel. 36, Last sequence update) 15-JUL-2004 (Rel. 44, Last annotation update) Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                         Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=XBRED21/12/93; TISSUE=Lymph node; MEDLINE=55337423; PubMed=7612930; Dunham S.P., Argyle D.J., Onions D.E.; Dunham S.P., Trip isolation and sequence of canine interleukin-2."; DNA Seq. 5:177-180(1995).
                                           GO; GO:0005576; C:extracellular; IEA.
GO; GO:000514; F:interleukin-2 receptor binding; IEA.
GO; GO:0005955; P:interleukin-2 receptor binding; IEA.
GO; GO:0006955; P:interleukin-2 IEA.
InterPro; IPR000779; 4 helix cytckine.
PITATE PRO00779; Interleukin-2.
PEIMTE; PR00265; INTERLEUKIN2.
PRODOM; PD003649; Interleukin-2; 1.
                                                                                                                                                                                                                                                                                                                        66 AA; 7389 MW; 22A893F79DA2AE47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      Score 107.5; DB 2
Pred. No. 2.8e-08;
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                                                                                                                                                                                                                                                                                                                                                       70.7%; Sco...
71.0%; Pred. No. 4...
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 APITSSSTKETEQQMEQLLLDLQLLLNGVNN 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AP-TSSSTKKTQLQLEHLLLDLQMILNGINN 31
EMBL; AF333117; AAK01437.1;
HSSP; P60568; 1IRL.
                                                                                                                                                                                                                                                                                                                                                                                                                       22; Conservative
                                                                                                                                                                                                                                                SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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152 AA
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                                   7 TSSSTKETEQQMEQLLLDLQLLLNGVNN 34
          TSSSTKKTQLQLEHLLLDLQMILNGINN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY247760; AAP04419.1;
HSSP; P60568; 1IRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Conservative
                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Peromyscus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IL2 RABIT
077620;
                                                                                                                                                                                                                                                                                                                                   Name=112;
            4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                              Q80XG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 28
IL2_RABIT
                                                                                                                                RESULT 27
          à
                                                셤
                                                                                                                                                                                   DDT REPRESENT OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ሯ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (By similarity) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eanis ramiliaris (UOS).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                           InterPro; IRR009079; 4 helix cytokine.
InterPro; IRR000779; Interleukin-2.
Pfam; PF00715; IL2; IL.
PRINTS; PR00265; INTERLEUKIN2.
ProDom; PR003649; Interleukin-2; I.
PROSTIE; SW00189; IL2; I.
PROSTIE; PR00424; INTERLEUKIN 2; I.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 107; DB 2; Length 79
Pred. No. 4.1e-08;
6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF091131; AAD46989.1; -.
HSSP; P60568; 11RL.
                                                                                                                                                                                                                                                                                                                                                                                                                        By similarity.

Interleukin-2.
O-linked (GalNMc. . .) (By By By Similarity.
M -> I (in Ref. 3).
Q -> R (in Ref. 3).
F -> Y (in Ref. 3).
L -> M (in Ref. 3).
C -> R (in Ref. 3).
Why in Ref. 3).
Why Dl23E486B7F4ACID CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO: 0005376; C: extracellular; IEA.
GO; GO: 0005134; F: interleukin-2 receptor binding; IEA.
GO; GO: 0005134; F: interleukin-2 receptor binding; IEA.
GO; GO: 000555; P: immune response; IEA.
InterPro; IPR000709; 4 helix cytokine.
InterPro; IPR000709; Interleukin-2.
PEam; PF00715; IL2; 1.
PRINTS; PR00255; INTERLEUKIN2.
SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 AA; 9087 MW; 83079BF8F8A659BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Interleukin-2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 107.5; DB 1
Pred. No. 7.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AP-TSSSTKKTQLQLEHLLLDLQMILNGINN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 APITSSSTKETEQQMEQLLLDLQLLLNGVNN 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00424; INTERLEUKIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17668 MW;
                                                                                                                           EMBL; U28141; AAA68969.1; -. EMBL; U11689; AAA75360.1; -. HSSP; P01585; 31NK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.7%;
71.0%;
                                                                                                    EMBL; D30710; BAA06378.1; -.
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Best Local Similarity 71.4%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 71.0<sup>1</sup>
Matches 22; Conservative
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155
24
112
127
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154
155 AA;
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NON TER
SEQUENCE
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CARBOHYD
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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Gaps
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MEDLINE-20304414; PubMed=10843729; DOI=10.1006/cyto.1999.0658;
Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
Perkins H.D., van Leeuwen G.H.-2, IL-4, IL-6 and IL-10 from the Buropean rabbit (Oryctolagus cuniculus).";
Cytokine 12:555-565(2000).
-!- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the
                                                                                                                                                                                                     Peromyscus maniculatus (Deer mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orycronagu cuniculus (madbil).
Bukaryotagu Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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15-JUL-1999 (Rel. 38, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schountz T., Buniger A., Davenport B., Hegg T., "Cloning of deer mouse IL-2, IL-12 p35, IL-21, GM-CSF, CCL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Match 70.4%; Score 107; DB 2; Length 152; Local Similarity 70.0%; Pred. No. 8.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:000576; C:extracellular; IEA.
GO; GO:0005134; P:interleukin-2 receptor binding; IEA.
GO; GO:0005134; P:interleukin-2 receptor binding; IEA.
GO; GO:000595; P:immune response; IEA.
InterPro; IPR00079; 4.helix_cytokine.
InterPro; IPR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
PRINTS; PR0015; IL2; 1.
PROSTIFS; PS00189; IL2; 1.
PROSTIFS; PS00424; INTERLEUKIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 152 AA; 17095 MW; 798D13514AD0CC93 CRC64;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Interleukin-2 (Fragment) 2.
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Query Match
Best Local Similarity 72.4
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                              NCBI_TaxID=42415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10036;
                                                                                                                                                                                                       Interleukin 2.
                                                                                                                                            Q923T2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 070329
                                                                                                                    RESULT 30
Q923T2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                         O-linked (GalNAc. . .) (By similarity). N-linked (GlcNAc. . .) (Potential).
         Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
"The complete cDNA sequences of IL-2, IL-4, IL-6 AND IL-10 from the European rabbit (Oryctolagus cuniculus).";
Cytokine 12:555-565(2000).
EMBL; AF169168; AAF86652.1;
 immune response. Can stimulate B cells, monocytes, lymphokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                            Cytokine; Glycoprotein; Growth factor; Immune response; Signal; T-cell.
                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Spleen;
MEDLINE=20304414; PubMed=10843729; DOI=10.1006/Cyto.1999.0658;
                                                                                                                                                                                                                                                                                                                                                                     Length 153;
                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                  By similarity.
8173536B2DDDBB86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00189; ILL2; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 133 AA; 14748 MW; 0D54758C190B5655 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR009079; 4 halix cytokine.
InterPro; IPR000779; Interleukin-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   Score 107; DB 1;
Pred. No. 8.6e-08;
                                                                                                                                                                                                                                                                                      By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 AA
                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                 Interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                   2 APTSSSTKKTQLQLEHLLLDLQMILNGINN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                21 APTSSSTKETQEQLDQLLLDLQVLLKGVND 50
                                                                                                                                                                         InterPro; IPR009079; 4 helix cytokine. InterPro; IPR000779; Interleukin-2. Pfam; PR0015; IL2; 1. PRINKIN2. PRODOM; PRODOM; PRODOM; PRODOM; PROPOM; PROPOM; PROPOM; PROPOM; PROPOM; PROPOM; PROPOM; PROSTIE; PS00424; INTERLEUKIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD003649; Interleukin-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin 2 variant IL2delta2.
                                                                                                                                                                                                                                                                                                                                  125 B
17256 MW;
                                                                                                                                                     EMBL; AF068057; AAC23838.1; -
                                                                                                                                                                                                                                                                                                                                                                  70.4%;
                                                                                                                                                                                                                                                                                                                                                                                           21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00715; IL2; 1.
                                                                                                                                                                   P01585; 1M4A.
                                                                                                                                                                                                                                                                                                                                              153 AA;
                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=IL-2;
                                                                                                                                                                                                                                                                                                           CARBOHYD
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                                                                               Gaps
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Darnell M.R., Pletneva L.M., Langley R.J., Blanco J.C., Prince G.A.;
Submitted (JuL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF398549; AAK94012.1; -.
HSSP; P60568; 1IRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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TISSUESpleen;
MEDILINE-89234044; PubMed=9573100;
Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
"Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and analysis of cytokine mRNA expression in experimental visceral leishmaniasis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interleukin-2 (Fragment).
Mesoricetus auratus (Golden hamster).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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                         Score 106; DB 2; Length 133;
                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
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PROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 155 AA; 17627 WW; ACADEA865E993291 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
PRINTS; PRO0265; INTERLEUKIN2.
                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.7%; Score 106; DB 2; 73.3%; Pred. No. 1.2e-07; iive 3; Mismatches 5;
                                                   le-07;
69.7%; Scor. 72.4%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                          155 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 APTSSSTKKTQLQLEHLLLDLQMILNGINN 31
                                                                                                                               2 APTSSSTKKTQLQLEHLLLDLQMILNGIN 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 APTSSSTKETQQHLEQLLLDLQVLLRGIKN
                                                                                                                                                              21 APTSSSTKETQEQLDQLLLDLQVLLKGVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sigmodon hispidus (Hispid cotton rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Infect. Immun. 66:2135-2142(1999).
BMBL; AF046212; AAC40097.1; -.
HSSP; RO5058; 11RL.
GO; GO:0005576; C:extracellular; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07. Last ROW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD003649; Interleukin-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Conservative
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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CARBOHYD
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=IL2;
                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                      PIG
                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                              RESULT 33
       FFFS
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                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chain mkNa..;
Immunogentics 30:145-147(1989).
-I- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the proliferation and other activities crucial to regulation of the proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.
-!-SUBGELLULAR LOCATION: Secreted.
-!-SUBILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McKnight A.J., Mason D.W., Barclay A.N., "Sequence of rat interleukin 2 and anomalous binding of a mouse interleukin 2 cDNA probe to rat MHC class II-associated invariant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IFR009079; 4 helix cytokine.
InterPro; IFR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
PROWINS; PR00265; INTERLEUKIN2.
PRODOM; PR003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
PROSTITE; PS00444; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
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01-AUG-1990 (Rel. 15, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
Name=112; Synonyms=11-2;
                                                                                                                                                                                                                                                                                                  67.8%; Score 103; DB 2; Length 138; 73.3%; Pred. No. 3e-07; ive 2; Mismatches 6; Indels
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR000709; J. 4.helix.cytokine.
InterPro; IPR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
PRIMTS; PR00265; INTERLEUKIN2.
SMART; SM00189; IL2; 1.
PROSTIE; PS00424; INTERLEUKIN-2; 1.
PROSTIE; PS00424; INTERLEUKIN_2; 1.
                                                                                                                                                                                                                                                       138 AA; 15739 MW; 351032995B670779 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 AA
                                                                                                                                                                                                                                                                                                                                                                                             2 APTSSSTKKTQLQLEHLLLDLQMILNGINN 31
                                                                                                                                                                                                                                                                                                                                                                                                                       14 APTSSSKKETQQHLEQLLLDLQELLKGINN 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89339608; PubMed=2788130;
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                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 73.3
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat)
                                                                                                                                                                                                                                    138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P01585; 1M49.
RGD; 620047; Il2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chain mRNA.";
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T-cell.
SIGNAL
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                    Query Match
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NON TER
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P17108;
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                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91274360; PubMed=2054386; DOI=10.1016/0167-4781(91)90019-I; Goodall J.C., Emery D.C., Bailey M., English L.S., Hall L.; "cDNA cloning of porcine interleukin 2 by polymerase chain reaction."; Biochim. Biophys. Acta 1089:257-258(1991).
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interleukin-2.
O-linked (GalNAc. . .) (By similarity).
y similarity.
; 67A8554A73BF30A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metăzoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0265; INTERLEUKIN2.
ProDom; PD0013649; Interleukin-2; 1.
SMART; SM00189; IL2; I.
PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
                                                                                                                          Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                          Score 97; DB 1; 1
Pred. No. 2.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                    154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                       50
                                                                                                                                                                                                                           2 APTSSSTKKTQLQLEHLLLDLQMILNGINN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X56750; CAA40071.1; -.
EMBL; X58428; CAA41330.1; -.
EMBL; AB041935; BAB16110.1; -.
EMR; S16241; S16241.
HSSP; P01585; 1M49.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR000779; Interleukin-2.
Pfam; PP00715; IL2; 1.
                                                                                                                                                                                                                                                     21 APTSSPAKETOOHLEOLLLDLOVLLRGIDN
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                          155 AA; 17632 MW;
                                                                                                                          63.8%;
                                                                                                                                               Local Similario,
nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
  155
23
126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scrofa (Pig)
  21
23
78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lefevre F.;
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Best Local Similarity 66.7
Matches 20; Conservative
                                                                                                                                                                                                                                                                              NCBI_TaxID=9844;
                                                                                                                                                                                                           Interleukin 2.
                                                                                                                                                                 01-JUN-2003
                                                                                                                                                                                01-JUN-2003
01-MAR-2004
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01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IL2 HORSE
P37997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                            RESULT 35
Q865X2
              Matches
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IL2_HORSE
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                                                                                                                         Gaps
          By similarity.
Interleukin-2.
O-linked (GalNAc. . .) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-54114702; PubMed=8128610; DOI=10.1016/0165-2427(94)90015-9; Mai Z., Kousoulas K.G., Horohov D.W., Klei T.R.; "Cross-species PCR cloning of gerbil (Meriones unguiculatus) interleukin-2 cDNR and its expression in COS-7 cells."; Vet. Immunol. Immunopathol. 40:63-71(1994).

-I-FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fmmune response. Can stimulate B cells, monocytes, lymphokine-
activated killer cells, natural killer cells, and glioma cells.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity)
                                                                                                                                                                                                                                                                                                                                               Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00424, INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
                                                                                                                          ö
                                                                                                                                                                                                                                                                         01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
                                                                                             63.2%; Score 96; DB 1; Length 154;
                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .) (By
                                                     By similarity.
F3B95E43D4A3D3E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     By similarity.
DOF74AA1A381CDDA CRC64;
                                                                                                          Pred. No. 3.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interleukin-2.
O-linked (GalNAc.
                                                                                                                                                                                                                                                    155 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
                                                                                                                         4; Mismatches
                                                                                                                                                                   21 APTSSTKNTKKQLEPLLLDLQLLLKEVKN 50
                                                                                                                                                    2 APTSSSTKKTOLOLEHLLLDLOMILNGINN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; POIS85; IM49.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
                                                                                                                                                                                                                                                    PRT;
                                                                  154 AA; 17401 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17602 MW;
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                                                                                                            66.78;
                                                                                                         Local Similarity 66.7 tes 20, Conservative
                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
155
23
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=10047;
                                                                                                                                                                                                                                                 IL2 MERUN
Q08081;
                                                    DISULFID
SEQUENCE
                                       CARBOHYD
                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
T-cell.
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             SIGNAL
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                          CHAIN
                                                                                                            Best Loc
Matches
STTTES
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62.5%; Score 95; DB 1; Length 155,

Query Match

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                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raadan O., Lee S.-., Yoshida R., Chang K.-., Ohashi K., Sugimoto C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94160538; PubMed=8116217; DOI=10.1016/0165-2427(93)90070-K; VandergriffE E.V., Horohov D.W.; Molecular cloning and expression of equine interleukin 2."; Vet. Immunol. Immunopathol. 39:395-406(1993).
                                                                                                                                                                                                                                                                                                                                             Lama glama (Llama).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Cetartiodactyla, Tylopoda, Camelidae, Lama.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1994 (Rel. 30, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TGGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.2%; Score 93; DB 2; Length 154
66.7%; Pred. No. 1.1e-05; Lindels
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Onuma M.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00424; INTERLEUKIN 2; 1.
SEQUENCE 154 AA; 17652 MW; 8020EC8DDB7BBA38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:000595; P:immune response; IEA.
InterPro; IPR009079; Jenix cytokine.
InterPro; IPR000779; Interleukin-2.
Prom; PR00715; IL2; I.
SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
5.5e-06;
8;
                                                                                                                                                                                                             154 AA
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                66.7%; Pred. No. 5.56
                                                                                                21 APTSSPAKEAQQYLEQLLLDLQQLLRGINN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 APTLSSTKDTKKQLEPLLLDLQFLLKEVNN 50
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                                                                          2 APTSSSTKKTQLQLEHLLLDLQMILNGINN
                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                               (TrEMBLrel. 24, (TrEMBLrel. 24, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB107651; BAC75388.1;
HSSP; P60568; 1IRL.
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                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Gaps

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Indels

Conservative

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Best Local Similarity
Matches 19; Conserv
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SEQUENCE
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                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, matural killer cells, and glioma cells.
--- SUBCELJULAR LOCATION: Secreted.
--- SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                          EMBL; L06009; AAA20134.1; -.

R EMBL; X63393; CAA49190.1; -.

R PIR; S31391; S31391.

R HSCP: P01585; IM39.

R InterPro; IPR00079; 4 helix_cytokine.

R InterPro; IPR00079; Interleukin-2.

R Pfan; PF00715; IL2; 1.

R PRINTS; PR00265; Interleukin-2; 1.

R SMART; SM00189; IL2; 1.

R SMART; SM00189; IL2; 1.

R PROSITE; PS00424; INTERLEUKIN 2; 1.

R PROSITE; PS00424; INTERLEUKIN 2; 1.

Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
                                                                                                                                                                                                                                                                                                                                                                         (By similarity).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93289963; PubMed=8512072; DOI=10.1006/abio.1993.1209; Mullner S., Karbe-Thonges B., Tripier D.; "Charge heterogeneity of insulin fusion proteins expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli is not due to proteolytic degradation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                              R -> K (in Ref. 2).
S -> A (in Ref. 2).
N -> D (in Ref. 2).
N -> D (in Ref. 2).
E -> G (in Ref. 2).
E -> G (in Ref. 2).
D -> K (in Ref. 2).
OSIBBBC47A0114FC CRC64;
                                                                                                                                                                                                                                                                                                                                    By similarity.
Interleukin-2.
By similarity.
O-linked (GalNAc. .) (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anal. Biochem. 210:366-373(1993).
SEQUENCE 23 AA; 2637 MW; 40B64C6875CE021F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UCF5;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 92; DB 1;
Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 APTSSSTKKTQLQLEHLLLDLQMILNGINN 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17086 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 56.7%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin 2 (Fragment).
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148
149 AA;
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CONFLICT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                          T-cell.
SIGNAL
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59.9%; Score 91; DB 2; Length 23;

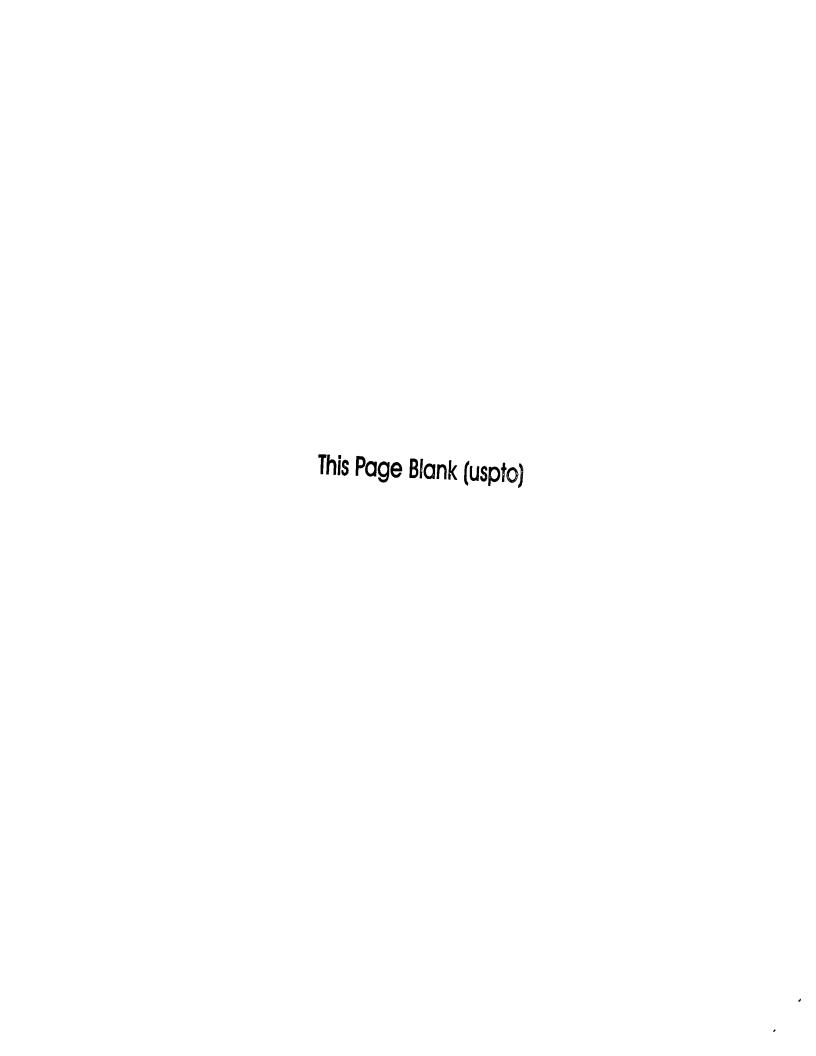
Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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-!- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokineactivated killer cells, natural killer cells, and glioma cells (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Cetacea, Odontoceti, Delphinidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Ness T.L., Bradley W.G., Reynolds J.E. III, Roess W.B.;
"Isolation and expression of the interleukin-2 gene from the killer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
T-cell. 1 20 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 By similarity.
>152 Interleukin-2.
23 O-linked (GalNAc. . .) (By
1126 By similarity.
152
1154 MW, 308F9182IECCB764 CRC64;
                      Pred. No. 2.6e-06; ); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
Interleukin-2.
O-linked (GalNAc..
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 88; DB 1;
Pred. No. 6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                                      152 AA
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or send an email to license@isb-sib.ch).
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InterPro; IRRO09079; 4 helix cytokine.
InterPro; IPR009079; Interleukin-2.
Pfam; PF00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
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90.5%; Prev
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Orcinus orca (Killer whale).
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nes 18; Conservative
                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                whale, Orcinus orca.";
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23 78 1
78 1
152 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                           071V48;
051V48;
05-JUL-2004 (TERBLrel. 27, Last sequence update)
05-JUL-2004 (TERBLrel. 27, Last annotation update)
105-JUL-2004 (TERBLICEL. 27, Last annotation update)
105-JUL-2004 (TERBLICEL. 27, Last annotation update)
1000 sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Delphinapterus leucas (Beluga whale).
Sukaryota; Metazota; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Cetacea; Odontoceti;
Monodontidae; Delphinapterus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    57.2%; Score 87; DB 2; Length 38; 100.0%; Pred. No. 1.8e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                            Turner D.M., Sinnott P.J., Hutchinson I.V.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF031845; ABB86681.1; -
GO; GO:0005776; C:extracellular; IEA.
GO; GO:0005134; R:interleukin-2 receptor binding; IEA.
GO; GO:0065955; P:immune response; IEA.
InterPro; IRR000779; Interleukin-2.
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SEQUENCE 154 AA; 17652 MW; 4288D3D41D04F172 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR000779; Interleukin-2.
                                                                                                                                                                                                                                                                                                                                                                                 NON TER 38 38 SEQÜENCE 38 AA; 4192 MW; 8DE4AE5344C2CBA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Vet. Immunol. Immunopathol. 67:385-394(1999).
EMBL; AP072870; AAD40847.1; -.
HSSP; P60568; 1IRL.
                                  38 AA.
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ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD003649; Interleukin-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Best Local Similarity 100.0
Matches 18, Conservative
                                PRELIMINARY;
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                                                                                                                                                                                 NCBI_TaxID=9606;
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Q9XT84
RESULT 39
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Search completed: September 23, 2005, 12:48:03 Job time : 55.8525 secs



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Compugen Ltd.
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Copyright (c) 1993 - 2005
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A;Residues: 1-153 <MAE>
A;Residues: 1-153 <MAE>
A;Cross-references: GB:J00264; NID:g186294; PIDN:AAD48509.1; PID:g5729676
A;Experimental source: tonsillar mononuclear cells
B;Experimental source: tonsillar mononuclear cells
B;Devos, R.; Plaetinck, G.; Cherource, H.; Simons, G.; Degrave, W.; Tavernier, J.; Remau.
Nucleic Acids Res. 11, 4307-4323, 1983
A;Title: Molecular cloning of human interleukin 2 cDNA and its expression in Escherichia A;Reference number: A93478; MUID:83246551; PMID:6306584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781
A;Experimental source: splenocytes
A;Experimental source: splenocytes
A;Exenberg, O.; Paber-Elman, A.; Lotan, M.; Schwartz, M.
J; Neurochem. 64, 1928-1936, 1995
A;Title: Interleukin-2 transcripts in human and rodent brains: possible expression by as
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R;Siebenlist, U.; Durand, D.B.; Bressler, P.; Holbrook, N.J.; Norris, C.A.; Kamoun, M.;
Mol. Cell. Biol. 6, 3042-3049; 1986
A;Title: Promoter region of interleukin-2 gene undergoes chromatin structure changes and A;Reference number: I57603; MUID:87064618; PMID:3491296
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A;Cross-references: GB:M22005; NID:g186300; PIDN:AAA59140.1; PID:g386818
A;Note: mutation of Phe-42 to Ala reduced binding to the IL-2 receptor 5-10 fold without
                                                                                                                                                           R.; Hamuro
                                                                                                            chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781
A;Experimental source: leukemic T-cell line, Jurkat-111, cloned from Jurkat-FHCRC
R;Macda, S.; Nishino, N.; Obaru, K.; Mita, S.; Nomiyama, H.; Shimada, K.; Fujimoto,
Biochem. Biophys. Res. Commun. 115, 1040-1047, 1983
A;Title: Cloning of interleukin 2 mRNAs from human tonsils.
A;Tetle: A90113; MUID:84023840; PMID:6312994
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A;Notecule type: mRNA
A;Notecule type: mRNA
A;Residues: 5-7, F', 9-17, P', 19-32, 'X', 34-45, 'X', 47-143 <RES>
A;Cross-references: GB:S77835; NID:g999001; PIDN:AAD14264.1; PID:g4261964
B;Nishinto, N.; Obaru, K.; Maeda, S.; Shimada, K.; Onoue, K.
Biomed. Res. 6, 197-205, 1985
A;Title: Organization of the DNA regions flanking the human interleukin 2 gene.
                                              A,Cross-references: EMBL:214955
A,Note: this sequence is shown from the beginning of the fragment to the chrom R,Taniguchi, T.; Mateui, H.; Fujita, T.; Takaoka, C.; Kashima, N.; Yoshimoto, Nature 302, 305-310, 1983
A,Title: Structure and expression of a cloned cDNA for human interleukin-2. A,Reference number: A93297; MUID:83167472; PMID:6403867
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R;Welr, M.P.; Chaplin, M.A.; Wallace, D.M.; Dykes, C.W.; Hobden, A.N.
Biochemistry 27, 6883-6892, 1988
A;Title: Structure-activity relationships of recombinant human interleukin 2.
A;Reference number: I52401; MUID:89063420; PMID:3264184
A;Contents: recombinant IL-2 and mutants expressed in B. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: 156518; MUID:95239150; PMID:7722480
A;Accession: 156518
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A;Molecule type: mRNA
A;Residues: 1-152 <EIZ>
A;Cross-references: GB:S77834; NID:g999000
A;Accession: I73624
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A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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A;Accession: I52528
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A; Residues: 1-153 < DEV>
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A; Residues: 1-153 <TAN>
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A; Residues: 1-68 <RE2>
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Proc. Natl. Acad. Sci. U.S.A. 82, 7284-7288, 1985

Proc. Natl. Acad. Sci. U.S.A. 82, 7284-7288, 1985

Aritile: A viral long terminal repeat in the interleukin 2 gene of a cell line that cons A; Reference number: A94067; MUID:86042650; PMID:3877307

A; Residues: 1-153 < CHE>
B; 1-153/Product: interleukin-2 #status predicted <112>
F; 21-153/Product: interleukin-2 #status predicted
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A.Molecule type: DNA
A.Cross-references: GB.J00264; NID:g186294; PIDN:AAD48509.1; PID:g5729676
R.Holbrook, N.J.; Smith, K.A.; Fornace Jr., A.J.; Comeau, C.M.; Wiskocil, R.L.; Crabtree Proc. Natl. Acad. Sci. U.S.A. 81, 1634-1638, 1884
A.Title: T-cell growth factor: complete nucleotide sequence and organization of the gene A.Reference number: A20961; MUID:84170356; PMID:6608729
A.Accession: A20961
A.Accession: A20961
A.Residues: 1-153 <4DO2>
A.Cross-references: GB:K02056; NID:g186302; PIDN:AAA98792.1; PID:g386819
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NAlternate names: IL-2, T-cell growth factor
C;Alternate names: IL-2, T-cell growth factor
C;Species: Homo sapiens (man)
C;Date: 11-Aug-1983 #sequence_revision 11-Aug-1983 #text_change 09-Jul-2004
C;Date: 11-Aug-1983 #sequence_revision 11-Aug-1983 #text_change 09-Jul-2004
C;Accession: Anola99; A21192; A20961; S31209; A93297; A90113; A93478; I56518; I73624; I52
R;Holbrook, N.J.; Lieber, M.; Crabtree, G.R.
Nucleic Acids Res. 12, 5005-5013, 1984
A;Fitle: DNA sequence of the 5' flanking region of the human interleukin 2 gene: homolog A;Accession: A01849
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A; Molecule type: DNA
A; Residues: 1-153 < HOL>
A; Cross-references: UNIPROT: P60568; GB:X00695; GB:X00200; GB:X00201; GB:X00202; NID:g337;
A; Fujita, T.; Takaoka, C.; Matsui, H.; Taniguchi, T.
R; Fujita, T.; Takaoka, C.; Matsui, H.; Taniguchi, T.
A; Full A; Gad. Sci. US.A. 80, 7437-7441, 1983
A; Title: Structure of the human interleukin 2 gene.
A; Reference number: A21192; MUID:84170243; PMID:6324170
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                                                                                                                                                                                               interleukin-2 precursor - common gibbon shifternate names: IL-2; T-cell growth factor species: Hylobates lar (common gibbon, white-handed gibbon) species: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004 spacession: A94067; A01849
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96.7%; Score 147; UB
Best Local Similarity 100.0%; Pred. No. 3.4
Matches 30; Conservative 0; Mismatches
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ALIGNMENTS
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A; Molecule type: mRNA
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interleukin-2 precursor - rat
NyAlternate names: IL-2; T-cell growth factor
C;Species Rattus norvegicus (Norway rat)
C;Date: 26-Apr-1989 #sequence_revision 26-Apr-1989 #text_change 09-Jul-2004
C;Accession: A45882; A31278
B;McKnight, A.J.; Mason, D.W.; Barclay, A.N.
Immunogenetics 30, 145-147, 1989
A;Title: Sequence of rat interleukin 2 and anomalous binding of a mouse interleukin 2 cl
A;Reference number: A45882; MUID:89339608; PMID:2788130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-155 <MCK>
A;Cross-references: UNIPROT:P17108; GB:M22899; NID:g204909; PIDN:AAA41427.1; PID:g204910
C;Superfamily: interleukin-2
C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell
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A; Residues: 1-154 <GOO>
A; Residues: 1-154 <GOO>
A; Crose-references: UNIPROT: P26891; EMBL: X56750; NID: g1991; PIDN: CAA40071.1; PID: g1992
R; Lefevre, F
Bubmitted to the EMBL Data Library, March 1991
A; Description: Molecular cloning of porcine interleukin 2 cDNA by the polymerase chain A; Reference number: $15473
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S33509
R;Mai, Z.; Klei, T.; Horohov, D.
submitted to the EMBL Data Library, October 1992
A;Description: Cross-species PCR cloning of Jird (Meriones unguiculatus) interleukin-2
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NyAlternate names: IL-2; T-cell growth factor
C;Species: Sus scroff adomestica (domestic pig)
C;Species: Sus scroff adomestica (domestic pig)
C;Accession: S16241; S15473
R;Goodall, J.C.; Emery, D.C.; Bailey, M.; English, L.S.; Hall, L.
Biochim. Biophys. Acta 1089, 257-258, 1991
A;Title: cDNA cloning of porcine interleukin 2 by polymerase chain reaction.
A;Reference number: S16241; MUID:91274360; PMID:2054386
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C;Superfamily: interleukin-2
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Pred. No. 7.7e-07;
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Matches 20; Conservative
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Best Local Similarity 66.7
Matches 20; Conservative
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A; Residues: 1-154 < LEF>
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                                                                                                                                                                  A, Accession: A94009
A, Molecule type: protein
A, Mote: disulfide bonds and carbohydrate binding site were determined
A, Note: heterogeneity in Jurkat-derived IL-2 is primarily due to differences in glycosyl
In lacking 21-Ala (FT-II2-A and FT-II2-B) and 22-Pro (FT-II2-B)
A, Numatz, M.: Dittmar, K.B.J.; Lindenmaier, W.; Hoppe, J.; Hauser, H.
J. Biol. Chem. 264, 17368-17373, 1989
A, Title: Expression of human interleukin-2 in recombinant baby hamster kidney, Ltk-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Accession: A34463
A.Molecule type: protein
A.Residues: 21-35 < CON>
A.Molecule type: protein
A.Residues: 21-35 < CON>
A.Molecule type: protein
A.Residues: 21-35 < CON>
B.Molecule type: protein
A.Residues: 21-35 < CON>
B.Molecule type: protein
A.Roter. Us. Hofer, B.; Nimtz, M.; Jaeger, V.; Conradt, H.S.
Bur. J. Biochem. 215, 189-197, 1993
A.Title: Biosynthesis and secretion of human interleukin 2 glycoproteins variants from hymeneric number: S34052; MUID:93345493; PMID:8344280
A.Contents: annotation; glycosylation of variant forms expressed in insect cells
A.Genetics:
A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Gene
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A;Map position: 4926-4927
A;Map position: 4926-4927
A;Introns: 49/3; 59/3; 117/3
C;Superfamily: interleukin-2
C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell F;1-20/Domain: signal sequence #status predicted <SIG>F:1-15/Pomain: signal sequence #status experimental <IL2>F:21-15/Pomain: aignal sequence #status experimental <IL2>F:21-15/Disulfide bonds: #status experimental
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C;Superfamily: interleukin-2
C;Keywords: growth factor
R;Robb, R.J.; Kutny, R.M.; Panico, M.; Morris, H.R.; Chowdhry, V. Proc. Natl. Acad. Sci. U.S.A. 81, 6486-6490, 1984
Proc. Natl. Acad. Sci. U.S.A. 81, 6486-6490, 1984
Pritle: Amino acid sequence and post-translational modification of human interleukin A;Reference number: A94009; MUID:85038540; PMID:6333684
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Cispecies: Pells silvestris catus (domestic cat)
Cispace: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
Cisccession: JN0698
R;Cozzi, P.U.; Padxid, P.A.; Takeda, J.; Alegre, M.L.; Yuhki, N.; Leff, A.R.
Biochem. Biophys. Res. Commun. 194, 1038-1043, 1993
A;Title: Sequence and functional characterization of feline interleukin 2.
A;Reference number: JN0698; MUID:93356765; PMID:8352761
A;Accession: JN0698
A;Status: nucleic acid sequence not shown
A;Residues: 1-154 <COZ>
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Pred. No. 2.4e-09;
5; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 APASSSTKETQQQLEQLLLDLRLLLINGVNN
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Best Local Similarity 73.3%;
Matches 22; Conservative
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Best Local Similarity 100. Matches 30; Conservative

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Query Match

interleukin 2 precursor - cat

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 ARIM-
A;Cross-references: UNIRROT:P36835; EMBL:X76063; NID:g416002; PIDN:CAA53664.1; PID:g4160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P19114; EMBL:X53934; NID:g1281; PIDN:CAA37881.1; PID:g1282 K;Seow, H.F.; Rothel, J.S.; Radford, A.J.; Wood, P.R. Nucleic Acids Res. 18, 7175, 1990 A; Mucleic Acids Res. 18, 7175, 1990 A; Mucleic Acids Res. 18, 7176, 1990 A; Mucleic Acids Res. 18, 7176, 1990 A; Mucleic Acids Res. 18, 7100 A; Mucleic Acids Res. 18, 7100 A; Mucleic Acids Res. 18, 7100 A; Reference number: S13102; MUID:91088336; PMID:2263496
                                                                                                                                                                                                                                            interleukin-2 - goat
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: Obs. 1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S38662
R;Rinstad, E.
Rsinstad, E.
Ribitted to the EMBL Data Library, November 1993
A;Bescription: The molecular cloning and expression of caprine interleukin 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interleukin-2 precursor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S11488; S130102; S15517
R;Goodall, J.C.; Emery, D.C.; Perry, A.C.F.; English, L.S.; Hall, L.
Nucleic Acids Res. 18, 5883, 1990
A;Title: CDNA cloning of ovine interleukin 2 by PCR.
A;Reference number: S11488; MUID:91016933; PMID:2216781
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-5,'L',7-155 <SEO>
A;Crosa-references: EMBL:X55641; NID:g1810; PIDN:CAA39165.1; PID:g1811
K;Bujdoso, R.; Williamson, M.L.; Sargan, D.R.; Hein, W.H.; McConnell, I.
submitted to the EMBL Data Library, April 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 155;
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0.00034;
...a 8; Indels
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0.00034;
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Pred. No. 0.00
6; Mismatches
                                      31
                                                                      21 APTSSSTGNTMKEVKSLLLDLQLLLEKVKN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 APTSSSTGNTMKEVKSLLLDLQLLLEKVKN 50
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A;Residues: 21-153 <BUJ>
A;Cross-references: EMBL:X60148
C;Superfamily: interleukin-2
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A;Accession: S15517
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Best Local Similarity
Matches 16; Conserv
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Matches 16; Conserv
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A; Residues: 1-155 <GOO>
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C;Date: 16-Aug-1996 #sequence revision 16-Aug-1996 #text_change 09-Jul-2004
C;Date: 16-Aug-1996 #sequence revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: 145913; 221470; 220761
R;Cerretti, D.P.; McKereghan, K.; Larsen, A.; Cantrell, M.A.; Anderson, D.; Gillis, S.; Proc. Natl. Acad. Sci. U.S.A. 83, 3223-3227, 1986
A;Title: Cloning, sequence, and expression of bovine interleukin 2.
A;Reference number: 145913; MUID:86205869; PMID:3517854
A;Accession: 145913
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Reduce: type: mRNA
A;Residues: 1-155 <CER>
A;CRS>
A;Cross-references: UNIPROT: POSO16; GB:M12791; NID:g163204; PIDN:AAA30586.1; PID:g163205
B;Anikeeva, N.N.; Vinogradova, T.V.; Votcohin, O.N.
Submitted to the EMBL Data Library, December 1989
A;Recence number: S21470
A;Molecule type: DNA
A;Recence number: S21470
A;Rocession: S21470
A;Rocession: S21470
A;Rocession: S21470
A;Rocession: S21470
A;Rocession: C;Genetics: EMBL:X17201; NID:g452; PIDN:CAA35062.1; PID:g453
                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 <MAI>
A;Cross-references: UNIPROT:Q08081; EMBL:X68779; NID:g577588; PIDN:CAA48679.1; PID:g3116
C;Superfamily: interleukin-2
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Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell
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A;Molecule type: mRNA
A;Residues: 1-149 < TRNA
A;Cross-references: UNIPROT:P37997; EMBL:X69393; NID:g1076; PIDN:CAA49190.1; PID:g1077
C;Superfamily: interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interleukin-2 precursor - horse
C;Species Equus caballus (domestic horse)
C;Species: Bquus caballus (domestic horse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 831391
R;Tavernor, A.S.; Butcher, G.W.
R;Tavernor, A.S.; Butcher, G.W.
R;Description: cDNA cloning of equine interleukin-2 by polymerase chain reaction.
A;Reference number: 831391
A;Accession: 831391
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                                                                                                                                                                                                                                         62.5%; Score 95; DB 2; Length 155; 66.7%; Pred. No. 1.5e-06; 1ive 2; Mismatches 8; Indels
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Pred. No. 0.00034;
6; Mismatches 8; Indels
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Best Local Similarity 53.3%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                      20; Conservative
A; Reference number: S33509
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Best Local Similarity
Matches 20; Conserv
                               A; Accession: S33509
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A,Accession: A94064
A;Molecule type: mRNA
A;Residues: 1-169 <VOK.
A;Residues: 1-169 <VOK.
A;Cross-treferences: GB:K02292; NID:g198330; PIDN:AAA39289.1; PID:g309404
A;Cross-treferences: GB:K02292; NID:g198330; PIDN:AAA39289.1; PID:g309404
R;Kabhima, N.; Nishi-Takaoka, C.; Fujita, T.; Taki, S.; Yamada, G.; Hamuro, J.; Taniguci Nature 313, 402-404, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X01772; GB:K02797; NID:g52663; PIDN:CAA25909.1; PID:g758159 C;Comment: Produced by T-cells in response to antigenic or mitogenic stimulation, this ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell F:1-20/Domain: signal sequence #status predicted <SIG> $721-169/Product: interleukin-2 #status predicted <MAT> F:23/Binding site: carbohydrate (Thr) (covalent) #status predicted F:92-140/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interleukin 2 - western wild mouse (fragment)
C;Species: Mus spretus (western wild mouse)
C;Species: Mus spretus (western wild mouse)
C;Date: O.2-Mug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: 168870
R;Matesanz, F.; Alcina, A.; Pellicer, A.
Immunogenetics 38, 300-303, 1993
A;Title: Existence of at least five interleukin-2 molecules in different mouse strains.
A;Reference number: 154512; MUID:93307791; PMID:8319981
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A;Cross-references: UNIPROT:Q08867; GB:L07575; NID:g349515; PIDN:AAA39327.1; PID:g34951
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Immunogenetics 38, 300-333, 1993
A;Title: Existence of at least five interleukin-2 molecules in different mouse strains.
A;Reference number: 154512; MUID:93307791; PMID:8319981
                                                                                                                                                                                                                               A,Title: Unique structure of murine interleukin-2 as deduced from cloned cDNAs.
A,Reference number: 148597; MUID:85111148; PMID:2578624
A,Accession: 148597
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C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
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A; Reference number: A94064; MUID:85113172; PMID:3918306
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Pred. No. 0.088;
                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.1%; Score 64; DB 1;
Best Local Similarity 38.6%; Pred. No. 0.061;
Matches 17; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: 154512
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Superfamily: interleukin-2
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                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-169 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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A; Status: preliminary
A; Accession: 837289
A; Status: preliminary
A; Modecule type: mRNA
A; Reference number: 53/289
A; Cross-references: UNIPROT:QBBHA4; EMBL:X73040
R; Matesanar, F.; Addina, A.; Pellicer, A.
B; Modecule bye: mew cDNA sequence for the murine interleukin-2 gene.
A; Reference number: 52/205; MUID:93041941; PMID:1420317
A; Rocession: 52/205
A; Molecule type: mRNA
A; Residues: 1-63 < MATE>
A; Roces-references: EMBL:X66058; NID:952725; PIDN:CAA46854.1; PID:952726
A; Ghosh, S; Palmer, S.M.; Rodrigues, N.R.; Cordell, H.J.; Hearne, C.M.; Cornall, R.J.;
R; Ghosh, S; Palmer, S.M.; Rodrigues, N.R.; Cordell, H.J.; Hearne, C.M.; Cornall, R.J.;
R; Accession: 33.6162
A; Status: preliminary
A; Residues: 1-50 < GHO>
A; Coss-references: EMBL:X73040
C; Superfainly: interleukin-2
C; Superfainly: interleukin-2
C; Superfainly: signal sequence #status predicted < SIG>
F; 21-63/Product: interleukin-2 #status predicted < NAT>
F; 20/Domain: signal sequence #status predicted < NAT>
F; 21-63/Product: interleukin-2 #status predicted < NAT>
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A;Molecule type: DNA
A;Residues: 1-169 < DEG>
A;Cotta: 1-169 < DEG>
A;Cotta: T.; Atai, N.; Lee, F.; Rennick, D.; Mosmann, T.; Atai, K.
Proc. Natl. Acad. Sci. U.S.A. 82, 68-72, 1985
A;Title: Use of a cDNA expression vector for isolation of mouse interleukin 2 cDNA clone
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A;Molecule type: DNA
Residues: 1-169 «FUS»
A;Cross.references: UNIPROT:P04351
R;Degrave, W.; Simons, G.; Devos, R.; Plaetinck, G.; Remaut, B.; Tavernier, J.; Fiers, Mol. Biol. Rep. 11, 57-61, 1986
A;Title: Cloning and structure of a mouse interleukin-2 chromosomal gene.
A;Reference number: A54490; MUID:86118396; PMID:3003564
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NyAlternate names: IL-2; T-cell growth factor (TCGF)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text change 09-Jul-2004
C;Accession: A93550; A54490; Ā94064; I48597; A01850; I84713
R;Fuse, A.; Fujita, T.; Yasumitsu, H.; Kashima, N.; Hasegawa, K.; Taniguchi, T. Nucleic Acids Res. 12, 9323-9331, 1984
A;Title: Organization and structure of the mouse interleukin-2 gene.
A;Reference number: A93550; MUID:85087940; PMID:6240025
                                                                                                                                                                                                   _revision 13-Jan-1995 #text_change 09-Jul-2004
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Pred. No. 0.011;
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                                                                                                                                                                                                                                   C;Accession: S37289; S27205; S36162; S24936
R;Todd, J.A.
submitted to the EMBL Data Library, April 1993
                                                                                                                            interleukin-2 precursor - mouse
C;Species: Mus muscullus (bouse mouse)
C;Date: 13-7an-1995 #sequence revision 13-Ja
C;Accession: S37289; S27205; S36162; S24936
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Best Local Similarity 47.2%;
Matches 17; Conservative
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A; Reference number: S09089; MUID: 90242961; PMID: 2110531
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Matches 9; Conserv
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A;Molecule type: DNA
A;Residues: 1-737 <HEI>
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NiAlternate names: acyl coenzyme A-6-aminopenicillanic acid acyltransferase; acyltransferase

NiAlternate names: acyl coenzyme A-6-aminopenicillanic acid acyltransferase; acyltransferase; cipacies: Emericella nidulans, Aspergillus nidulans acid acyltransferase; acyltra
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C;Accession: 168871
E;Accession: 168871
Immunogenetics 38, 300-303, 1993
A;Title: Existence of at least five interleukin-2 molecules in different mouse strains. A;Reference number: 154512; MUID:93307791; PMID:8319981
A;Accession: 168871
A;Accession: 168871
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-72 <RES>
A;Cross-references: GB:L07576; NID:g349517; PIDN:AAA39328.1; PID:g349518
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C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
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A;Molecule type: DNA
A;Residues: 1.62 <RES>
A;Cross-references: GB:L07574; NID:g349513; PIDN:AAA39326.1; PID:g349514
C;Genetics:
A;Gene: Il-2
C;Superfamily, 'nterman's 'nterman
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Pred. No. 0.21;
5; Mismatches 5; Indels
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38.5%; Score 58.5; DB 2;
Best Local Similarity 42.9%; Pred. No. 0.13;
Matches 15; Conservative 6; Mismatches 5;
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Best Local Similarity 35.6
Matches 16; Conservative
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C;Superfamily: interleukin-2
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A,Accession: F64145
A,Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-155 <TIGR>
A,Cross-references: UNIPROT:P44583; GB:U32709; GB:L42023; NID:g1573190; PIDN:AAC21897.1;
A,Note: best homolog was a hypothetical protein from Escherichia coli
C,Superfamily: hypothetical protein H10227
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C;Species: Vibrio cholerae
C;Accession: G8226
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
R;Heidelberg, J.F.; Eisen, J.A.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
R.R.; McMalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
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A;Experimental source: serogroup Ol; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein H10227 - Haemophilus influenzae (strain Rd KW20)
Cispecies: Haemophilus influenzae
Cispecies: Haemophilus Radms, M.D.; Mams, M.A.; Kirkness, B.F.; Kerlavage, R.Fleischmann, R.D.; Alrichay, J.M.; Maidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
Ajauthors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350610; PMID:7542800
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                                                                                                                                                                                                                                                        Length 357;
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                                                                                                                                                                                                                                                        DB 2;
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Pred. No. 3.2;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAPTSSSTKKTQLQLEHLLLDLQMILNGINN 31
                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                        Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                8 TKKTOLOLEHLLLDLOMIL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                40 TKKTQAELEQLLRELEQVM 58
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29.0%;
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Best Local Similarity 52.6%;
Matches 10; Conservative
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Best Local Similarity 39.4%;
Matches 13; Conservative 4
A; Accession: 809090
A; Molecule type: protein
A; Residues: 103-122 < WHI>
C; Genetics:
A; Introns: 12/3; 71/1; 121/3
C; Keywords: acyltransferase
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: C70701
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, E.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Ralandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Accession: C70701
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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C;Species: Vibrio cholerae
C;Species: Vi
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: F82217
R;Heidelberg, Jr.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methyl-accepting chemotaxis protein VC1298 [imported] - Vibrio cholerae (strain N16961
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                                                                                                       hypothetical protein Rv0029 - Mycobacterium tuberculosis (strain H37RV)
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Pred. No. 16;
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Best Local Similarity 40.09
Matches 12; Conservative
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                      probable LyaR-type regulator [imported] - Sinorhizobium meliloti (strain 1021) magaplasm C;Species: Sinothizobium meliloti
C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: F9228
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe C;Accession: F9228
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe J; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9889, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Retence number: A95262; MUID:213661469; PIDN:AAK64848.1; PID:g14523262; GSPDB:GA;Retence number: A: Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, A;Retence sumpler: A: Davis, R.W.; Dreano, S.; Rederspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 299, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; M. M.L.; M.L.; M. M.L.; M.L.; M. M.L.; M. M.L.; M. M.L.; M. M.L.; M. M.L.; M. M.L.; M.L.; M.M.L.; M.L.; M.M.L.; M.L.; M.L.; M.L.; M.L.; M.L.; M.L.; M.L.;
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C;Date: 13-Peb-198 #sequence_revision 13-Peb-1998 #text_change 09-Jul-2004
C;Date: 13-Peb-1998 #sequence_revision 13-Peb-1998 #text_change 09-Jul-2004
C;Accession: E70122
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, U.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Son, D.; Peterson, U.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Son, D.; Porter, Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Scension: E70122
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: L-627 <KLE>
A;Cross-references: UNIPROT:P70859; GB:AE001129; GB:AE000783; NID:g2688071; PIDN:AAC6657
A;Experimental source: strain B31
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                                                      Query Match
33.6%; Score 51; DB:
Best Local Similarity 48.1%; Pred. No. 9.5;
Matches 13; Conservative 5; Mismatches
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    PTSSSTKKTQLQLE----HLLLDLOMILNGINN
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Query Match
Best Local Similarity 44.0°
Matches 11; Conservative
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Best Local Similarity
Matches 9; Conserv
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Cidate: 10-Way-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
Cidate: 10-Way-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
Cidate: 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99065613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1130 <STO>
A;Crossreferences: GB:chr_V; PIDN:AAB37038.1; PID:gl086805; GSPDB:GN00023; CESP:F52E1.4
C;Genetics:
A;Gene: F52E1.4
A;Map position: 5
C;Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain home
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID:20406833; PMID:10952301
A; Accession: F82217
A; Molecule type: DNA
A; Residues: 1-543 <HBI>A; CHOSENTE CONSTRUCT: Q9KSF8; GB:AE004209; GB:AE003852; NID:99655779; PIDN:AAF9445
A; CROSS-references: UNIPROT: Q9KSF8; GB:AE004209; GB:AE003852; NID:99655779; PIDN:AAF9445
C; Genetics:
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A;Reference number: 219530
A;Accession: T2210
A;Accession: T2210
A;Molecule type: DNA
A;Residues: 1-240 <WIL>
A;Cross-references: UNIPROT:Q20417; EMBL:Z49910; PIDN:CAA90123.1; GSPDB:GN00020; CESP:F4
C;Genetics:
C;Genetics:
A;Gene: CESP:F4464.7
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Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
Accession: A89130
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C;Species: Caenorhabditis elegans
C;Date: 15-Cct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22210
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A;Introns: 123/2; 159/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F44G4.7
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36;
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32.2%; Score 49;
Best Local Similarity 46.2%; Pred. No. 9
Matches 12; Conservative 6; Mismatcl
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Pred. No.
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Best Local Similarity 37.5%;
Matches 9; Conservative
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A,Map position: 1
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C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: H64307
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Ritle: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
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A;Accession: Abl37

A;Authors: Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.

; Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

b.; Jones, L.M.; Karset, U.

Science 294, 4849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUD:21537279; PMID:11679669

A;Accession: AB1367

A;Atatus: preliminary

A;Atatus: preliminary

A;Residues: 1-441 < GLA>
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A;Experimental source: strain EGD-e
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB1367
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                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein MJ0064 - Methanococcus jannaschii
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      DB 2;
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31.9%; Score 48.5; E
44.0%; Pred. No. 17;
tive 9; Mismatches
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PTSSQEQREKWRVK-LLIDLEMILS
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C'Superfamily: pol polyprotein
Kreywords aspartic proteinase; hydrolase; nucleotidyltransferase; polyprotein; reverse
F;111-210/Product: retropepsin #status predicted <RTP>
F;134/Active site: Asp (shared with dimeric partner) #status predicted
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86548
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2311, 2010.
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SPBC21D10.13 SPBC1921.07c – fission yeast (Schizosaccharomyces pom
        A;Accession: B30045
A;Molecule type: DNA
A;Residues: 1-1061 <FUK>
A;Comment: Specific enzymatic cleavages may yield mature proteins including protease,
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A;Molecule type: DNA
Residues: 129-244 <SE2>
A;Cross-references: EMBL:AL122033; PIDN:CAB58973.1; GSPDB:GN00067; SPDB:SPBC1921.07c
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A; Cross-references: UNIPROT:Q9USW9; EMBL:AL031536; NID:e1319499
A; Cross-references: UNIPROT:Q9USW9; EMBL:AL031536; NID:e1319499
B; Experimental source: strain 972h(-)
B; Experimental source: strain 972h(-)
B; Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL bara Library, October 1999
A; Reference number: Z21816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB 1; Length 100. Pred. No. 1.1e+02;
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A; Reference number: A30045; MUID:88232906; PMID:3374586
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Best Local Similarity 52.9%;
Matches 9; Conservative
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Matches 11; Conser
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-938 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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                                                                                           C; Species: Listeria innocua (Sincera Innocua (Sincera) - Libreria (Sincera) - Libre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV-1 retropepsin (EC 3.4.23.16) - simian immunodeficiency virus (African green monkey in NiContains: endounclease (EC 3.1.-.); retropepsin (EC 3.4.23.16); RNA-directed DNA poly C; Species is imian immunodeficiency virus, SIV (C; Date: 30-Unn-1989 #sequence_revision 30-Unn-1989 #text_change 03-Unn-2002 (C; Accession: B30045 #sequence_revision 30-Unn-1989 #text_change 03-Unn-2002 R; Pkukasawa, M.; Miura, T.; Hasegawa, A.; Morikawa, S.; Tsujimoto, H.; Miki, K.; Kitamura Nature 333, 457-461, 1988 **
A; Title: Sequence of simian immunodeficiency virus from African green monkey, a new memb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G protein-coupled neuropeptide pyrokinin-2 receptor (CG8795) - fruit fly (Drosophila mellor, Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Accession: JC8012
R; Rosenkilde, C.; Cazzamali, G.; Williamson, M.; Hauser, F.; Sondergaard, L.; DeLotto, R B; Accession: Biophys. Res. Commun. 309, 485-494, 2003
A; Ricference number: JC8011; PMID: 12951076
A; Reference number: JC8011; PMID: 12951076
A; Residues: 1-595 < ROS>
A; Residues: 1-595 < ROS>
A; Residues: 1-595 < ROS>
C; Comment: This receptor is a G protein-coupled receptor and a transmembrane protein as effecting, and behavior.
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A.Introns: 115/1; 170/2; 214/3; 281/1; 352/3; 390/3
C.Keywords: G protein-coupled receptor; neuropeptide pyrokinin; transmembrane protein
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                                                                  aminopeptidase C [imported] - Listeria innocua (strain Clip11262)
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C;Superfamily: aminopeptidase C (bleomycin hydrolase)
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7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :: || :| :| | 344 TAMTKAERLDYKHSMLTHAMVLTGVN 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 SSSTKKTQLQLEHLLLDLQMILNGIN 30
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Best Local Similarity 34.6%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymorphic membrane protein E/F family CP0286 [imported] - Chlamydophila pneumoniae (st C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (c)Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (c)Species: Chlamydophila pneumoniae, Chaccession: H72074; E81593 #Sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C;Accession: H72074; E81593 H3999 #text_change 09-Jul-2004 R;Kalman, S: Mitchell, W: Marathe, R: Lammel, C: Fan, J: Olinger, L.; Grimwood, J:; Nature Genet. 21, 385-389, 1999 A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUD:99206606; PMID:10192388 A;Recssion: H72074 A;Residues: 1-938 cARN> A;Reference number: A81500; MUD:20150255; PMID:10684935 A;Reference number: A81500; MUD:20150255; PMID:10684935 A;Residues: 1-938 cREA> A;Residues: 
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R;Fraser, C.M.; Casjons, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Son, D.; Peterson, J.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: B70209
A;Accession: B70209
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-398 «KLE>
A;Cross-references: UNIPROT:050911; GB:AE000790; NID:g2690224; PIDN:AAC66245.1; PID:g269
A;Cross-references: UNIPROT:Q9Z883; GB:BA000008; NID:g8978836; PIDN:BAA98772.1; GSPDB:GN
E,Experimental source: strain J138
C;Genetics:
A;Gene: pmp_15
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C;Superfamily: Lyme disease spirochete plasmid conserved hypothetical protein BBG06
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C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 1.1e+02;
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Pred. No. 1.1e+02;
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31.2%;
Best Local Similarity 42.9%;
Matches 12; Conservative
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Best Local Similarity 42.99
Matches 12; Conservative
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hypothetical protein SA0640 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: O-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Joace: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Joace: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
Ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q99VT6; GB:BA000018; PID:g13700576; PIDN:BAB41873.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA0640
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1008 <LTN>
A; Residues: 1-1008 <LTN>
A; Cross-references: UNIPROT: Q9UU99; EMBL: AL109608; PIDN: CAB51563.1; GSPDB: GN00068; SPDB: A; Experimental source: strain 972h-; cosmid c23B6
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F;639-822/Domain: cellular retinaldehyde-binding protein homology <CRB>
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                Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 557;
                                                              12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.9%; Score 47; DB 2; Le
larity 32.0%; Pred. No. 1.4e+02;
Conservative 7; Mismatches 10;
                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
30.9%; Sco...
40.7%; Pred. No. 50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                      4 TSSSTKKTQLQLEHLLLDLQMILNGIN 30
                                                                                                                                 Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | :|| : ||: ||: ||: PARQNTKTSPLQIRHLVFSLECAID 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.9%;
58.8%;
                                                    11; Conservative
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              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-557 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: F89839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 37
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Search completed: September 23, 2005, 12:48:58 Job time : 27.3934 secs
                                                                                                   Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-466 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: E90228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: SS00786
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C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2004
C;Accession: A59282
R;Bhati.Dey, N.; Taira, M.; Conti, M.A.; Nooruddin, H.; Adelstein, R.S.
Mech. Dev. 78, 33-36, 1998
A;Title: Differential expression of non-muscle myosin heavy chain genes during Xenopus e A;Reference number: A59282; MUID:99077683; PMID:988676
A;Reference number: A59282; MUID:99077683; PMID:988676
A;Accession: A59282
A;Accession: A59282
A;Accession: A59282
A;Accession: A59282
A;Accession: MNRAP: O99252; GB:AF055895; NID:G3660671; PIDN:AAC83556.1; PID:G366
C;Superiamental source: cell line XTC
C;Superfamily: myosin heavy chain; myosin motor domain homology
F;84-764/Domain: myosin motor domain homology <a href="https://www.neaps.com/motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-motor-moto
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T05656
R;Bevan, M; Wedler, H; Kutzner, M; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F
Submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15420
A;Reference number: Z15420
A;Accession: T05656
A;Molecule type: DNA
A;Residues: 1-159 < ABEV>
A;Residues: 1-159 < ABEV>
A;Cross-references: UNIPROT: Q9SVP7; EMBL: AL035539
A;Experimental source: cultivar Columbia; BAC clone F22113
C;Genetics:
A;Anap position: 4
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C;Accession: C84888

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197
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A;Molecule type: DNA
A;Residues: 1-211 <STO>
A;Cross-references: UNIPROT:022147; GB:AE002093; NID:g2583136; PIDN:AAB82645.1; GSPDB:GN
C;Genetics:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A;Note: F22113.50
C;Superfamily: Arabidopsis thaliana hypothetical protein F22113.50
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30.6%; Score 46.5; DB 2; Length 159;
Best Local Similarity 46.4%; Pred. No. 21;
Matches 13; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 30.9%; Score 47; DB 2; Length 1964; Best Local Similarity 42.9%; Pred. No. 3e+02; Matches 12; Conservative 2; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 TSSSTKKTQLQLEHLLLDLQMILNGINN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 PTSSSTKKTQLQLEHLLLDLQMILNGIN 30
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C;Accession: E90228
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandog, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandog, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Earmett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Pescription: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q9UXH3; GB:AE006641; NID:g13813962; PIDN:AAK41084.1; GSPDB:C
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                amino acid specific permease [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May_2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
                                                                                                                       Gape
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C; Superfamily: Arabidopsis thaliana hypothetical protein F22113.50
                                                             Length 211;
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Best Local Similarity 38.1%; Pred. No. 70;
Matches 16; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAPTSSSTKKT---QLQLEHLLLDLQMILN-----GINN 31
                                                             DB 2;
                                                          Score 46.5; Pred. No. 29;
                                                                                                              3; Mismatches
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                                                    30.6%;
nilarity 46.4%;
Conservative
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